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The invention comprises an antibody that specifically binds a regeneration IV (Reg IV) protein. The invention specifically comprises the amino acid and coding sequences of single chain antibody fragments (scr. 8) that bind Reg IV protein. The antibody of the invention is useful for treating, preventing and ameliorating: inflammatory bowel disorders (e.g. ulcerative colitis or Crohn's disease), diabetes (e.g. non-insulin dependent diabetes or insulin dependent diabetes), and cancer of the gastrointestinal tract. The antibody of the invention is also useful for detecting the expression of a Reg IV protein. The present DNA sequence represents a PCR primer that was used to amplify a Reg IV-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              testis-specific tubulin tyrosine-ligase-like polypeptide;
BGS-42 polypeptide; cytostatic; respiratory-Gen; gastrointestinal-Gen;
neuroprotective; endocrine-Gen; antiinflammatory; anabolic; hypertensive;
osteopathic; nootropic; antiparkinsonian; antiarthritic; antiasthmatic;
anti-HIV; antibacterial; immnosuppressive; antiseborrheic;
dermatological; tyrosine ligase modulator; gene therapy; tubulin ligase;
tubulin-carboxypeptidase; cellular proliferation; reproductive disorder;
testicular disorder; testicular cancer; pulmonary disorder; lung cancer;
gastrointestinal disorder; colon cancer; stomach cancer; neural disorder;
small intestine; brain; lymph tissue; infertility; Cushing's syndrome;
emphysema; pneumonia; Addison's disease; acromegaly; Alzheimer's disease;
Parkinson's disease; immunological disorder; arthritis; asthma; AlDS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New testis-specific tubulin tyrosine-ligase-like BGS-42 polypeptide, useful for preventing, treating or ameliorating a medical condition, eaberrant cellular proliferation, reproductive disorders or testicular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sepsis; acne; Sjogren's disease; scleroderma; human; PCR; primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Match 0.5%; Score 17.2; DB 1; Length 23; Local Similarity 86.4%; Pred. No. 1.1e+03; les 19; Conservative 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 23 BP; 3 A; 3 C; 12 G; 5 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human BGS-42 protein-related PCR primer SegID69.
                                   Example 2; SEQ ID NO 137; 324pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          853 CAGGAGCTGGTGGAGGCTG 874
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (BRIM ) BRISTOL-MYERS SQUIBB CO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             09-JUL-2003; 2003WO-US021605.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        09-JUL-2002; 2002US-0394725P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Feder JN, Wu S, Nelson TC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADJ93418 standard; DNA; 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       06-MAY-2004 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5-JAN-2004.
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IID ADJ9

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This invention relates to a novel testis-specific tubulin tyrosine-ligase
-like polypeptide, designated the BGS-42 polypeptide. The invention may
come useful for the development of compounds with a cytostatic, respiratory
Gen, gastrointestinal-Gen, neuropotective, endocrine-Gen,
antiinflammatory, anabolic, hypertensive, osteopathic, nootropic,
antiinflammatory, anabolic, hypertensive, osteopathic, nootropic,
antiinflammatory antiseborrheic or dermatological activity acting as
tyrosine ligase modulators. In addition, the disclosed sequences may be
compared for diagnosing a pathological condition, or a susceptibility to a
useful for gene therapy. The BGS-42 polypeptide or polymuclectide can be
useful for diagnosing a pathological condition, as a disorder related to aberrant
compared for diagnosing a subject, and for preventing, treating or
ameliorating a medical condition, such as a disorder related to aberrant
compared as activity, aberrant cellular proliferation, reproductive
disorders, testicular disorders, testicular cancer, pulmonary disorders,
carboxypeptidase activity, aberrant cellular proliferation, reproductive
disorders, testicular disorders, testicular cancer, pulmonary disorders,
cubulan lidase activity, aberrant cellular proliferation, reproductive
disorders, brain cancer, liver cancer, proliferative condition
of the testis, lung, small intestine, brain or lymph tissue. The BGS-42
polypeptide can be used as a preventive agent for immunological
disorders including arthritis asthma, AIDS, sepsies, acromegaly, Alchiemer's disease, or Parkinson's disease, or Parkinson's disease or scleroderma. The antibodise may be used to purify, disease or scleroderma. The antibodise may be used to purify, detect and
custor the BGS-42 polypeptides. The present sequence is that of a PCR
custor.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            albumin fusion protein; cytostatic; antianaemic; antiarthritic; antiasthmatic; anti-HIV; immunosuppressive; antinflammatory; antiasterial; osteopathic; dermatological; antigout; immunomodulator; antiarrhythmic; cardiant; nootropic; antilipaemic; nephrotropic; uropathic; neuroprotective; antiparkinsonian; tranquilizer; antidiabetic; anabolic; hypertensive; vulnerary; gene therapy; cancer; reproductive system disorder; primer; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 17.2; DB 1; Length 23;
Pred. No. 1.1e+03;
0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 23 BP; 3 A; 3 C; 12 G; 5 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human heavy variable primer, Hu VH3 5'.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    853 GAGGAGGAGCTGGTGGAGGCTG 874
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADL76556 standard; DNA; 23 BP
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25-APR-2000; 2000US-0199384P.
21-DEC-2000; 2000US-0256931P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12-APR-2001; 2001US-00833245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 86.4%;
Matches 19; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US2004010134-A1.
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Rosen CA, Haseltine WA;

Example 34; SEQ ID NO 69; 343pp; English

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activities: cytostatic, antianaemic, antiarthritic, antiacthmatic, activities: cytostatic, antianaemic, antiarthritic; antiacthmatic, antianaemic, activities: cytostatic, antianaemic, antiarthritic, antiacthmatic, antianaemic, and vulnerary. The albumin fusion protein nucleic acid may be used in gene therapy to treating, preventing or ameliorating diseases or disorders comprising indication: Y. The diseases or disorders include: cancer (e.g. leukaemia, colon, bone, breast, liver or lung cancer), immune or haematopoietic diseases (e.g. anaemia, Hodgkin's disease, acute immune or haematopoietic diseases (e.g. prostatitis, inguinal extra varicoccele, penile carcinoma, ovarian adenocarcinoma or Sertoli-leydig tumours), musculoskeletal disease, gout, muscular dystrophy cardiacaerse, haer valve disease, systemic lupus erythematosus, gout, muscular dystrophy arrhythmia, cardiac arrest, heat valve disease, hypernatraemia or payandrome or Tay Sandrome, Patanaemia), mixed foetal disease (e.g. rhabdomyomas, heart disease, carchexia), cardiac arrest, heat valve disease, hypernatraemia or Tay Sandrome, Patana syndrome, Turnary incontinence, urinary carchial artherism or renal diseases (e.g. urinary incontinence, urinary continents at alterial actions or renal diseases, cerebral meningitis, and action and ac
                                                                                                                                                                                                                                                                                                   The invention relates to a novel albumin fusion protein. The invention further relates to: a composition comprising the albumin fusion protein and a pharmaceutical carrier; a kit comprising the composition of the albumin fusion protein formula; a method of treating a disease or disorder in a patient comprising the step of administering the albumin fusion protein; a method of treating a patient with a disease or disorder that is modulated by Therapeutic protein: X, or its fragment or variant; a method of extending the shelf life of Therapeutic protein: X, or its fragment or variant; a nucleic acid molecule comprising a polynucleotide sequence encoding the albumin fusion protein; a vector comprising the nucleic acid molecule of the albumin fusion protein. The albumin fusion protein and a host cell albumin fusion protein and its compositions have the following
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cereballar ataxia, attention deficit disorder, autism or obsessive compulsive disorder), respiratory disease (e.g. emphysema, lung cancer or occupational lung disease), endocrine diseases (e.g. diabetes, Addison's disease or glomerulonephritis), digestive diseases (e.g. portal hypertension, irritable bowel disease, gastric atrophy or pancreatitis) or connective tissue or epithelial diseases (e.g. crohn's disease, scleroderma, wound healing or epidermolysis bullosa). This polynucleotide sequence represents a primer used in the exemplification of the
                                                                                                  New albumin fusion proteins, useful for diagnosing, treating, preventing
                                                                                                                                      or ameliorating diseases or disorders e.g. cancer, anemia, arthritis,
asthma, inflammatory bowel disease or Alzheimer's disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 23 BP; 3 A; 3 C; 12 G; 5 T; 0 U; 0 Other;
                                                                                                                                                                                                                                            Example 60; SEQ ID NO 38; 279pp; English
                             WPI; 2004-090519/09.
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853 GAGGAGCTGGTGGAGGCTG 874
                            1 gaggrecageregregaerere 22
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                                                                                                         ADN49125 standard; DNA; 23
                                                                                                                                                                  (first entry)
                                                                                                                                                                  29-JUL-2004
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                                                                           RESULT 735
                                                                                         ADN49125
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                                                                                                                                                                      Gaps
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                                                                                                                                    ch 0.5%; Score 17.2; DB 1; Length 23; I Similarity 86.4%; Pred. No. 1.1e+03; 19; Conservative 0; Mismatches 3; Indels
                                                                                                                                                                                                 853 GAGGAGGAGCTGGTGGAGGCTG 874
                                                                                                                                                                                                                              BP.
                                                                                                                                                                                                                                                                                                         23
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                                                                                                                                       Query Match
Best Local Similarity
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Best Loca Matches

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ADL22837; RESULT 734
ADL22837
ID ADL2283
XX
AC ADL2283

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                                                                       PCR; human; C3a receptor; antiasthmatic; antiallergic; cardiovascular; antiinflammatory; antiarthritic; receptor; antirheumatic; dermatological; immunosuppressive; vulnerary; antimicrobial; cytostatic; ss; primer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New isolated antibody that specifically binds C3a Receptor, useful for preventing, detecting, diagnosing, treating or ameliorating asthma, allergy, rheumatoid arthritis, systemic lupus erythematosus, arthritis or proliferative disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention relates to an isolated antibody that specifically binds the C3a Receptor, and which is shown in the specification. The antibody is useful for preventing, detecting, diagnosing, treating or ameliorating asthma, allergy, inflammatory or immune disorders. It is also useful for treating, preventing or ameliorating rheumatoid arthritis, systemic lupus erythematosus, arthritis, immunological hypereensitivities, physical trauma, organ transplant rejection, infectious diseases, cardiovascular disorders or proliferative disorders. The present sequence is a PCR primer used to amplify the coding sequence of a VH domain of an antibody directed at the human C3a receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               G-protein coupled receptor; GPCR; BMSOTR; therapy; G-protein coupled signalling; oxytocin-related disorder; eneutological disorder; spinal cord injury; ischaemia; infarction; cardiovascular disorder; acute heart failure; pancreatic cancer; diabetes mellitus; pancreatitis; immune-related disorder; HIV infection; asthma; metabolic disorder; endocrinal disorder; Cushing's syndrome; hyperthyroidism; genetic syndrome; Down's syndrome; Klinefelter's syndrome; Turner's syndrome; human; VH; PCR; primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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0
                                     Anti-human C3a receptor antibody VH domain PCR primer VH3-5'.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0.5%; Score 17.2; DB 1; Length 23; 86.4%; Pred. No. 1.1e+03; rive 0; Mismatches 3; Indel8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human VH gene amplifying PCR primer, Hu VH3-5'.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 2; Page 162; 199pp; English.
                                                                                                                                                                                                                                                                                                 31-JUL-2003; 2003WO-US023826.
                                                                                                                                                                                                                                                                                                                                    02-AUG-2002; 2002US-0400057P.
                                                                                                                                                                                                                                                                                                                                                                             (HUMA-) HUMAN GENOME SCI INC.
(first entry)
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Matches 19; Conservative
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                                                                                                                                                                                                                   WO2004013287-A2.
                                                                                                                                                                                Homo sapiens.
  20-MAY-2004
                                                                                                                                                                                                                                                          12-FEB-2004
                                                                                                                                                                                                                                                                                                                                                                                                                     Rosen CA;
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                                                                                                                                       antibody
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                                                                                                                                                                                                                                                                                                                                     The invention relates to novel methods for producing polypeptide-tagged collections and capture systems containing the tagged polypeptides. The method is useful for evenly distributing tags among members of a starting library. The system, collection, kits and methods are useful in developing pharmaceuticals and diagnostics. The present sequence is used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention relates to a method for the capture and analysis of biological particle using a capture system. The method is useful for
                                                                                                                                                                                              Evenly distributing tags among members of a starting library, useful in developing pharmaceuticals and diagnostics, comprises dividing the starting library into sub libraries and attaching a tag to members of each sub library.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Capturing biological particles, by contacting biological particles with capture system comprising addressed loci, addressed collection of polypeptide tagged molecules, capture agents, and polypeptide tag to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 17.2; DB 1; Length 23;
Pred. No. 1.1e+03;
0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kumble KD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Seguence 23 BP; 3 A; 3 C; 12 G; 5 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                   Disclosure, SEQ ID NO 14; 510pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQ ID 14.
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                                                                                                                                                                                                                                                                                                                                                                                                                                           in the exemplification of the invention.
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                                                                                                                   Geysen MH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           874
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           853 GAGGAGGAGCTGGTGGAGGCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Capture system related primer,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BP.
                30-OCT-2002; 2002US-0422923P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30-OCT-2002; 2002US-0422923P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 86.4%;
Matches 19; Conservative
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                                                                                                                   Atkinson B,
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                                                                           (POIN-) POINTILLISTE INC
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                                                                                                                                                         WPI; 2004-376185/35.
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                                                                                                                   Ault-Riche D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ault-Riche D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21-MAY-2004.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 737
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to G-protein coupled receptor (GPCR) BMSOTR and its corresponding nucleic acid sequence. GPCR is useful for diagnosing, preventing, treating or ameliorating a medical condition such as disorder related to aberrant G-protein coupled signalling, oxytocin-related disorders, neurological disorders e.g. spinal cord injuries, ischaemia, infarction, etc., disorder related to aberrant cell cycle regulation, cardiovascular disorders such as acute heart failure, disorder of the pancreas e.g. pancreatic cancer, diabetes mellitus, pancreatitis, alcohol asthma, etc., metabolic disorders, endocrinal disorders e.g. Ulvinfections, asthma, etc., metabolic disorders, endocrinal disorders e.g. Cushing's syndrome, hyperthyroidism, etc., mitochondrial DNA aberrations and syndrome, etc. The present sequence is a PCR primer used for amplifying human VH gene. This sequence is used in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                 Novel isolated human G-protein coupled receptor BMSOTR polypeptide and its variant, useful for diagnosing and treating neurological disorders such as spinal cord injuries or ischemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0.5%; Score 17.2; DB 1; Length 23; ilarity 86.4%; Pred. No. 1.1e+03; Conservative 0; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 23.BP; 3 A; 3 C; 12 G; 5 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                        Feder J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 13; SEQ ID NO 17; 97pp; English.
                                                                                                                                                                                                                                                                                                                      Mintier GA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             853 GAGGAGGAGCTGGTGGAGGCTG 874
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                                                                                                                   L2-MAR-2003; 2003US-00334360
                                                                                                                                                       04-JAN-2002; 2002US-0345706P
06-FBB-2002; 2002US-0355559P
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                                                                                                                                                                                                                                                                                                                      Gopal S,
                                                                                                                                                                                                                     RAMANATHAN C S.
                                                                                                                                                                                                                                      GOPAL S.
MINTIER G A.
FEDER J.
                                                                                                                                                                                                                                                                                                                                                              WPI; 2004-356195/33.
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                                     US2004086881-A1
                                                                                                                                                                                                                                                                                                                      Ramanathan CS,
Homo sapiens.
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                                                                             06-MAY-2004
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(MINT/)
                                                                                                                                                                                                                     RAMA/)
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RESULT 736

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vivlemore401-10.rng

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membranes, viruses, viral capsids, viral particles, bacterial cells, eucharlular compartments, organelles and micelles, prokaryotic cells, eucharlular compartments, organelles and micelles, prokaryotic cells, eucharbotic cells, intracellular particles, nuclei, cell membranes, cell membrane fragments, nuclear membranes fragments, viral capsids with or without packaged nucleic acid, phage, phage vectors or viral capsids with or without encapsulated nucleotide acid, liposomes and other micellar agents. The biological particles are cells, incurons, cancer cells, bacterial cells and infected cells, subcellular compartment, organelles, viral particles or pathogens. The cells neutons, cancer cells, bacterial cells or pathogens. The cells are dendritic cells, T cells, or B cells. The method is also useful for identifying molecules that interact with for identifying a modulator of an interaction among proteins in the trafficking, activity or functional or structural property in the biological particle, for identifying molecules that modulates the biological particle, and for mapping epitopes of molecules displayed on the surface of a biological particles, for identifying a receptor on the surface of a biological particle that transduces a signal from a polypeptide, and continue molecule that interacts with an apically continued molecule that interacts with an apically continued molecule molecule molecule and interacts with an apically continued molecule molecule that interacts with an apically continued molecule molecule molecule molecules displaced molecules and continued molecules and interacts with an apically continued molecule molecule molecule molecules and molecules and continued molecules and interacts with an apically continued molecule molecule molecule molecules and molecules
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Pred. No. 1.1e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 23 BP; 3 A; 3 C; 12 G; 5 T; 0 U; 0 Other;
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Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                illustrate the invention
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Oligodeoxyribonucleotide, intersubunit linkage; phosphoramidate intersubunit; antisense activity; nuclease resistant; in-vitro cell growth inhibition assay; infection; smooth muscle cell proliferation disorder; inflammatory process;
                                                                 Modified DNA oligonucleotide of the invention.
                  AAX59719 standard; DNA; 24 BP
                                                                                                                   genetic disorder; cancer; ss
                                                  (first entry)
                                                 22-JUL-1999
                                                                                                                                  Synthetic.
                                AAX59719;
RESULT 738
AAX59719
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Oligo:nucleotide N3'-P5' phosphoramidate(s) - have improved resistance toward phosphodiesterase digestion, and form stable duplexes with DNA and RNA strands.
                                                                                                                                                    Chen J;
                                                                                                        (LYNX-) LYNX THERAPEUTICS INC.
95WO-US003575
                                         94US-00210505
94US-00214599
                                                                                                                                                    Schultz RG,
                                                                                                                                                                                               WPI; 1995-344627/44.
                                                                                                                                                    Gryaznov SM,
20-MAR-1995;
                                      18-MAR-1994;
18-MAR-1994;
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W09525814-A1

28-SEP-1995.

Disclosure; Page 54; 101pp; English.

nucleoside subunits joined by intersubunit linkages, where at least 3 contiguous subunits are joined by phosphoramidate intersubunits. The contiguous subunits are joined by phosphoramidate intersubunits. The contiguous subunits are joined by phosphoramidate intersubunits. The coligodeoxyribonucleotides has a sequence of nucleoside subunits effective to form a duplex with a target nucleic acid molecule. The coligodeoxyribonucleotides are more resistant to nuclease digestion and have improved RNA and dsDNA hybridisation characteristics, relative to oligonucleotides not containing N3·P5' phosphoramidate linkages. They also have excellent antisense activity against complementary mRNA targets in in-vitro cell growth inhibition assays. They also exhibit low cytcoxicity. They may be used in diagnostic and therapeutic applications, e.g., in combatting infections agents such as bacteria, viruses, ect. or in treatment of smooth muscle cell proliferation disorders, inflammatory processes, certain genetic disorders, cancers, etc. . The present sequence represents an oligonucleotide of the invention Oligo:nucleotide N3'-P5' phosphoramidate(s) - have improved resistance toward phosphodiesterase digestion, and form stable duplexes with DNA and /*tag= a /note= "each base is linked by N3'-P5' phosphoramidate linkages" 1. .10
/*tag= a
/note= "each base is linked by N3'-P5' phosphoramidate phosphoramidate intersubunit, antisense activity, nuclease resistant, in-vitro cell growth inhibition assay, infection; smooth muscle cell proliferation disorder; inflammatory process; Gaps .. 0 specification describes oligodeoxyribonucleotides having Modified oligonucleotide containing N3'-P5' phosphoramidates. 0.5%; Score 17.2; DB 1; Length 24; 86.4%; Pred. No. 1.1e+03; tive 0; Mismatches 3; Indels Seguence 24 BP; 10 A; 0 C; 0 G; 14 T; 0 U; 0 Other; Oligodeoxyribonucleotide; intersubunit linkage; 2823 TATATATACATATATATATA 2844 Location/Qualifiers 3 TATATATTTTTATATATA 24 Chen J; (LYNX-) LYNX THERAPEUTICS INC. AAX59721 standard; DNA; 24 BP 94US-00210505. 94US-00214599. genetic disorder; cancer; ss 22-JUL-1999 (first entry) linkages" Schultz RG, 19; Conservative WPI; 1995-344627/44. Query Match Best Local Similarity modified base modified base W09525814-A1 20-MAR-1995; 18-MAR-1994; 18-MAR-1994; Gryaznov SM, 28-SEP-1995 Synthetic. AAX59721; Matches AAX5972. ò g

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                                                 The specification describes oligodeoxyribonucleotides having contiguous nucleoside subunits joined by intersubunit linkages, where at least 3 contiguous subunits are joined by phosphoramidate intersubunits. The coligodeoxyribonucleotides has a sequence of nucleoside subunits effective coligodeoxyribonucleotides as a sequence of nucleoside subunits effective to form a duplex with a target nucleic acid molecule. The coligodeoxyribonucleotides are more resistent to nuclease digestion and have improved RNA and dabNA hybridisation characteristics, relative to oligonucleotides not containing N3'-P5' phosphoramidate linkages. They also have excellent antisense activity against complementary mRNA targets in in-viro cell growth inhibition assays. They also exhibit low cytotoxicity. They may be used in diagnostic and therapeutic cytotoxicity. They may be used in diagnostic and therapeutic applications, e.g., in combatting infections agents such as bacteria, viruses, etc. or in treatment of smooth muscle cell proliferation disorders, inflammatory processes, certain genetic disorders, cancers, etc. The present sequence represents an oligonucleotide of the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TCR V-alpha and V-beta rearrangements were studied in 16 MS brains and in 10 control brains. TCRValpha-Jalpha-Calpha and Vbeta-Dbeta-Dbeta-Calpha rearrangements were confirmed with Southern blotting and hybridisation of the PCR product obtained by amplification with one of 18 Valpha or 21 of Vbeta specific oligonucleotide primers. See AAQ15052-92 for Valpha, Vbeta, Calpha and Cbeta primers. (Updated on 25-MAR-2003 to correct PA field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Method for diagnosing T-cell associated disease - comprises identifying rearranged variable region of appropriate T-cell also T-cell compsns. for treating neo:proliferative conditions.
                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TCR; multiple sclerosis; MS; brain; amplification; primer; ss.
                                                                                                                                                                                                                                                                                                              Score 17.2; DB 1; Length 24; Pred. No. 1.1e+03;
                                                                                                                                                                                                                                                                                                                                          3; Indels
                                                                                                                                                                                                                                                                                  Sequence 24 BP; 10 A; 0 C; 0 G; 14 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                         0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                     2823 TATATATACATATATATATA 2844
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                           Disclosure; Page 57; 101pp; English
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                                                                                                                                                                                                                                                                                                                                                                                      3 TATATATTTTTATATATA 24
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                                                                                                                                                                                                                                                                                                              0.5%;
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                                                                                                                                                                                                                                                                                                                                         19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (revised)
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                                                                                                                                                                                                                                                                                                                            Local Similarity
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19-FEB-1992
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAQ15061;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rat; melanocortin receptor; probe; dopamine; striatum; human; primer; PCR; amplification; expression vector; cardiovascular; renal; motor; neurological; psychiatric; gastro-intestinal; neuro-endocrinal; arterial hypertension; disturbed intestinal function; secretory disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New rat and human melanocortin receptor MC-5 - and related nucleic acid, transformed cells etc. useful for screening cpds. and for diagnosis and treatment of e.g. cardiovascular disease.
                                                                                                                   Gaps
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                                                            Length 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Facchinetti P;
                                                                                                                Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rat melanocortin receptor MC-5 amplification primer #3.
   0 Other;
                                                   Query Match

0.5%; Score 17.2; DB 1;
Best Local Similarity 86.4%; Pred. No. 1.1e+03;
Matches 19; Conservative 0; Mismatches 3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mignon V, Diaz J,
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C; 7 G; 3 T; 0 U;
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                                                                                                                                                                         2240 ACCCTGCTGCTGGTGCACAGCC 2261
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        dysfunction; adrenal gland; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       anomalies of the MC-5 receptor
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                                                                                                                                                                                                                                                                                                                                                   AAQ97706/c
ID AAQ97706 standard; cDNA; 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    06-FEB-1996 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sokoloff P,
   Sequence 24 BP; 5 A; 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Griffon N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ouery Match
Best Local S
Matches 19
                                                                                                                                                                                                                                                                                                                                                                                                                                           AAQ97706;
                                                                                                                                                                                                                                                                                                                        RESULT 741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
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AAT33122;

RESULT 742

AAT33122/

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Van Haringen H, Van Haringen WA;
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                                                                                                                                 BV.
                                                                03-MAR-2000; 2000EP-00200757.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   03-MAR-2000; 2000EP-00200757
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 03-MAR-2000; 2000EP-00200757
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (VHAE-) VAN HAERINGEN LAB BV
                                                                                                03-MAR-2000; 2000EP-00200757
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                 (VHAE-) VAN HAERINGEN LAB
                                                                                                                                                                                                   WPI; 2001-572636/65.
EP1130114-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unidentified.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EP1130114-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10-DEC-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAD17598;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 744
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention concerns an anti-Tie (Tyrosine kinase-Immunoglobulin like domain-EGF (epidermal growth factor) homology domain) monoclonal antibody (MAD) which specifically recognises the Tie extracellular domain, and a hybridoma producing it. The MAD can be used in the diagnosis of leukaemia and also in separation and concentration of haematopoietic stem cells. The MAD can also be used to detect and determine levels of (soluble) Tie. AAT33121-22 are primers used to amplify a 160 bp probe based on a tyrosine kinase domain, to detect the human Tie gene from a UT-7 cDNA library. A 3933 bp cDNA clone, ptk-1, was identified, encoding a 1138 amino acid residue protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Genomic DNA analysis; 5' variation generator; 3' fragment generator; endangered animal identification; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Anti-Tie monoclonal antibody and hybridoma producing it - useful in diagnosis of leukaemia and detection of haematopoietic stem cells.
                                                                                                                                                                              anti-Tie monoclonal antibody; extracellular domain; hybridoma; Tyrosine kinase-Immunoglobulin like domain-EGF homology domain; epidermal growth factor; leukaemia; diagnosis; separation; haematopoietic stem cells; detection; primer; probe; PCR; amplify; polymerase chain reaction; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0.4%; Score 17; DB 1; Length 17;
100.0%; Pred. No. 8e+02;
ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5' variation generator oligonucleotide PCR primer #11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 17 BP; 5 A; 6 C; 4 G; 2 T; 0 U; 0 Other;
                                                                                                                                                    3' primer to amplify 160 bp probe for Tie gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 1; Page 5; 19pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                          (YAMA ) YAMANOUCHI PHARM CO LID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1765 GAGGCCTTGTTTGACCG 1781
                                                  AAT33122 standard; DNA; 17 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAD17596 standard; DNA; 17 BP
                                                                                                                                                                                                                                                                                                                                                                                         94JP-00308249.
                                                                                                                                                                                                                                                                                                                                                                                                                           94JP-00308249.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17 GAGGCCTTGTTTGACCG 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                     07-NOV-1996 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1996-318959/32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                         JP08143598-A.
                                                                                                                                                                                                                                                                                                                                                                                         17-NOV-1994;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                           17-NOV-1994;
                                                                                                                                                                                                                                                                                                                                                          04-JUN-1996
                                                                                                                                                                                                                                                                                         Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAD17596;
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743

RESULT 74 AAD17596

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Matches

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The patent discloses a method and associated kit for analysing genomic DNA in a sample. The method comprises conducting a nucleic acid semplification on the genomic DNA in the sample using both first and second oligonuclectide primer to produce DNA fragments based on repeat sequences on at least one end of the genomic DNA. The first primer is a formation generator including a repeat sequence and at least one non-repeat nucleotide. The second oligonucleotide primer is a 3 fragment generator starting within such a genetic distance that amplification of the genomic DNA can be performed and preferably includes inosine. The method is useful for the genetic analysis of an individual organism, particularly of a species or individual. It is also useful for the rapid and straight forward identification of endangered animals or plants. The
                                                                                                                                                                                  Analyzing genomic DNA in a sample, useful for analyzing genes of organisms (e.g. a species or individual) or identifying endangered animals or plants, by using oligonucleotide primers comprising universal variable fragments.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             professional forward identification of endangered animals or plants. present DNA sequence is a 5' variation generator oligonucleotide PCR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Genomic DNA analysis; 5' variation generator; 3' fragment generator; endangered animal identification; PCR primer; 88.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ó,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ouery Match

0.4%; Score 17; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 8e+02;
Matches 17; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5' variation generator oligonucleotide PCR primer #13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 17 BP; 0 A; 1 C; 8 G; 8 T; 0 U; 0 Other;
Van Haringen H, Van Haringen WA;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 1; Page 6; 23pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2317 CTGTGTGTGTGTGTG 2333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAD17598/c
ID AAD17598 standard; DNA; 17 BP.
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Example; Col 14; 49pp; English.

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The patent discloses a method and associated kit for analysing genomic DNA in a sample. The method comprises conducting a nucleic acid amplification on the genomic DNA in the sample using both first and second oligonuclectide primer to produce DNA fragments based on repeat sequences on at least one end of the genomic DNA. The first primer is a 5' variation generator including a repeat sequence and at least one norrepeat nucleotide. The second oligonucleotide primer is a 3' fragment generator starting within such a genetic distance that amplification of the genomic DNA can be performed and preferably includes inosine. The method is useful for the genetic analysis of an individual organism, particularly of a species or individual. It is also useful for the rapid and straight forward identification of endangered animals or plants. The
                                                                  Analyzing genomic DNA in a sample, useful for analyzing genes of organisms (e.g. a species or individual) or identifying endangered animals or plants, by using oligonuclectide primers comprising universal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               present DNA sequence is a 5' variation generator oligonucleotide PCR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 17 BP; 8 A; 8 C; 1 G; 0 T; 0 U; 0 Other;
                                                                                                                                                                                          Example 1; Page 6; 23pp; English.
                       WPI; 2001-572636/65.
                                                                                                                                            variable fragments.
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0.4%; Score 17; DB 1; Length 17; 100.0%; Pred. No. 8e+02; cive 0; Mismatches 0; Indels 2318 TGTGTGTGTGTGTGC 2334 17 rerererererererer Best Local Similarity 100. Matches 17; Conservative

AAD34803 standard; DNA; 17 BP AAD34803; 745

Human FGFR3 allele detecting sense PCR primer. 16-JUL-2002 (first entry)

Human, chondrodysplasia, achondroplasia, transgenic mouse, therapy; fibroblast growth factor receptor 3; FGFR3; limb, midface hypoplasia; large skull; drug screening; drug development; transgenic; PCR; primer;

Ното варіепв.

US6265632-B1.

24-JUL-2001

99US-00383630. 98IL-00125958. 26-AUG-1999;

27-AUG-1998;

(YEDA) YEDA RES & DEV CO LI (PROC-) PROCHON BIOTECH LTD.

Yayon A, Segev O;

WPI; 2001-463946/50.

New transgenic mice having a genetically modified fibroblast growth factor receptor gene, useful as a model for human chondrodysplasia, e.g. achondroplasia characterized by shortening of the limbs, midface hypoplasia or large skull.

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The invention relates to an animal model for chondrodysplasia, more transgenic mouse model for achondroplasia. This transgenic mouse contains a fibroblast growth factor receptor 3 (FGFR3) gene including a G to A point mutation changing Gly to Arg in codon 380 in its genome. The transgenic mouse is useful as a model for FGFR-ssociated chondrodysplasia, particularly FGFR3 achondroplasia, e.g. shortening of the limbs, midface hypoplasia and large skull. This model may be exploited to gain better understanding of the disease and as an experimental model with which experimental therapy to chondrodysplasias can be exercised. The transgenic mouse is particularly useful as a tool for screening, developing and evaluating drugs with a potential of relieving or abolishing chondrodysplasia syndromes and/or symptoms. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          present sequence is a PCR primer used to detect human FGFR3 allele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 17 BP; 3 A; 5 C; 6 G; 3 T; 0 U; 0 Other;
\overset{\circ}{\times}\overset{\circ}{\times}\overset{\circ}{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\ci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Gaps ; 0 Query Match

0.4%; Score 17; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 8e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 455 CCTGCGTCGTGGAGAAC 471 1 cerecercerceacaac 17 셤 ઠે

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AADSS412 standard; DNA; 17 RESULT 746 AAD55412

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Gaps

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BP.

Human FGFR-3 DNA specific forward PCR primer. 07-AUG-2003 (first entry) AAD55412;

Human; antisense; fibroblast growth factor receptor 3; prophylaxis; developmental disorder; hyperproliferative disorder; antisense therapy; FGFR-3; ACH; JTK4; CEK2; cancer; PCR; primer; ss.

Homo sapiens.

WO2003023004-A2

20-MAR-2003.

06-SEP-2002; 2002WO-US028549.

(ISIS-) ISIS PHARM INC.

10-SEP-2001; 2001US-00953047.

Monia BP, Wyatt JR;

WPI; 2003-313244/30.

Novel compound targeted to a nucleic acid molecule encoding fibroblast growth factor receptor 3, useful for inhibiting the expression of the receptor and for treating an animal having cancer or developmental

Example 13; Page 76; 120pp; English.

The invention relates to antisense compounds targetted to a nucleic acid molecule encoding fibroblast growth factor (FGF) receptor 3 (also known as FGFR-3) ACH, TYK4 and CEK2) to inhibit its expression. Antisense compounds of the invention are useful for treating diseases or conditions associated with FGFR-3 such as developmental disorders or hyperproliferative disorders, especially cancer of colorectal, bladder, bone, lung, cervical, breast or skin. They are useful as research reagents, therapeutics, prophlylaxis, kits and diagnostics, and as tools in differential and/or combinatorial analyses to elucidate expression

vivlemore401-10.rng

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The sequence is that of a bovine microsatellite sequence obtd. by screening a library of bovine MboI DNA fragments of between 250 and 500 by with an (AGL)15 and a (TC)15 oligonucleotide probe. One out of 50 clones cross-hybridised. Assuming independent distribution of microsatellites and MboI sites, the frequency of (T6)n >9 microsatellites in the bovine genome is estimated at >100, 000. The sequence information in the bovine phovine microsatellite sis summarised in the sequence information specification and indexed herein (see below). The sequence information consistence of the microsatellite sequence were used to generate the microsatellite (using the program OPTIPRIM). The microsatellites may be used to identify individuals, for parentage testing, and in the genetic mapping of economic trait loci, or genes involved the determinism of economically important traits esp. in cattle, to allow selective breeding. See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN
                                                                                                                                                                                                                                                                                                                            ö
patterns of a portion of the genes expressed within cells and tissues. They are also useful in antisense therapy. The present sequence is human FGFR-3 DNA specific PCR primer. This primer is used in the exemplification of the invention
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                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage; genetic mapping; traits; amplification; ss.
                                                                                                                                                                                                                                                 0.4%; Score 17; DB 1; Length 17;
100.0%; Pred. No. 8e+02;
cive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 18 BP; 0 A; 0 C; 9 G; 9 T; 0 U; 0 Other;
                                                                                                                                                                                 Sequence 17 BP; 4 A; 5 C; 5 G; 3 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          a microsatellite from clone TGLA69.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   mapping, and selective breeding.
                                                                                                                                                                                                                                                                                                                                                                                            1245 GGCCATCGGCATTGACA 1261
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                                                                                                                                                                                                                                                                                                                                                                                                                                       1 GGCCATCGGCATTGACA 17
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Best Local Similarity 100.0
**** Conservative
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(first entry)
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02-FEB-1993
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AAQ34125

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The sequence is that of a bovine microsatellite sequence obtd. by screening a library of bovine Mbol DNA fragments of between 250 and 500 by with an (AC)15 and a (TC)15 oligonucleotide probe. One out of 50 clones cross-hybridised. Assuming independent distribution of microsatellites and Mbol sites, the frequency of (T6)n >9 microsatellites in the bovine genome is estimated at >100, 000. The sequence information for ca. 230 such bovine microsatellites is summarised in the specification and indexed herein (see below). The sequences upstream and downstream of the microsatellite sequence were used to generate the required PCR primers for in vitro amplification of the corresp.

microsatellite (using the program OPTIPRIM). The microsatellites may be used to identify individuals, for parentage testing, and in the genetic mapping of economic trait loci, or genes involved the determinism of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             economically important traits esp. in cattle, to allow selective breeding. See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN field.)
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                                                                                                                                                                                                                                            Microsatellite sequence from clone TGLA141.
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2335 GIGIGIGIGIGIGIG 2351
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                                                                                                                     AAQ33722 standard; DNA; 18 BP.
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(first entry)
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nes 17; Conservative
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02-FEB-1993
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0.4%; Score 17; DB 1; Length 18; 100.0%; Pred. No. 8.6e+02; ive 0; Mismatches 0; Indels

Best Local Similarity 100. Matches 17; Conservative

Query Match

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repeat_region
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10-MAR-2003
23-DEC-1993
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    Bos taurus.
                                                                                  06-AUG-1992
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The sequence is that of a bovine microsatellite sequence obtd. by
screening a library of bovine Mbol DNA fragments of between 250 and 500
by with an (AC)15 and a (TC)15 oligonuclectide probe. One out of 50
clones cross-hybridised. Assuming independent distribution of
microsatellites and Mbol sites, the frequency of (T6)n >9 microsatellites
in the bovine genome is estimated at >100, 000. The sequence information
for ca. 230 such bovine microsatellites is summarised in the
specification and indexed herein (see below). The sequences upstream and
comnstream of the microsatellite sequence waset to generate the
required PCR primers for in vitro amplification of the corresp.
microsatellite (using the program OPTIPRIM). The microsatellites may be
used to identify individuals, for parentage testing, and in the genetic
mapping of economic trait loci, or genes involved the determinism of
connectally important traits esp. in cattle, to allow selective
breding. See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN
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                                                                                                                                          PCR; selection; primers, OPTIPRIM; breeding; cattle; parentage; genetic mapping; traits; amplification; ss.
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                                                                                                   Microsatellite sequence from clone TGLA346.
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                                         (revised)
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                                      25-MAR-2003
02-FEB-1993
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02-FEB-1993
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  AAQ33950;
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AAQ33997
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creening a library of bovine Miol DNA fragments of between 250 and 500 by with an (AC)15 and a (TC)15 oligonucleotide probe. One out of 50 clones cross-hybridised. Assuming independent distribution of microsatellites and MboI sites, the frequency of (T6)n >9 microsatellites in the bovine genome is estimated at >100, 000. The sequence information for ca. 230 such bovine microsatellites is summarised in the specification and indexed herein (see below). The sequence information for ca. 230 such bovine microsatellite sequence were used to generate the required PCR primers for in vitro amplification of the corresp.

To sed to identify individuals, for parentage testing, and in the genetic mapping of economic trait loci, or genes involved the determinism of economic ally important traits esp. in cattle, to allow selective

Directing See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN
                                                                                                                                                                                                                                                                                                                                                                    Polymorphic bovine DNA markers - used in genetic identification, gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Table 7; Page 329; 517pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                               mapping, and selective breeding.
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92WO-US000340.
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/note= "SSR"
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(first entry)
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                                                                                                                                               GENM-) GENMARK.
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This (CA)9 simple sequence repeat is used to illustrate the novel method for detecting SSR polymorphisms without the need for direct sequencing or gel electrophoresis. The length of a particular repeat region (i.e. number of repeats) can be highly polymorphic; the sequences flanking repeat region, however, are conserved. Detection of a SSR of a specific length is achieved by successful ligation of two oligonucleorides, one being exactly complementary to the repeat region and one of its conserved flanking sequences and the other being complementary to the other conserved flanking sequence. (Updated on 10-MAR-2003 to add missing OS field.) (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Treating bacterial infections in humans or animals with oligo:nucleotide(s) - resistant to nuclease and targetted to bacterial nucleic acid or proteins, also conjugates of these oligo:nucleotide(s) with antibiotics.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nuclease resistant antisense oligo NBT 141 targeted against (AC)9.
                                                                                                                               Detecting genetic variation between organisms - by detecting polymorphisms in simple sequence repeats in DNA of organisms
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nuclease resistant; bacterial infection; antibiotic; target; veterinary medicine; treatment; human; industrial process; bacterial control; ss.
                                                                                                                                                                                                                                                                                                                                                                                              0.4%; Score 17; DB 1; Length 18;
100.0%; Pred. No. 8.6e+02;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                    Sequence 18 BP; 9 A; 9 C; 0 G; 0 T; 0 U; 0 Other;
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                                                                                                                                                                            Disclosure; Page 5; 8pp; English.
                                        (PION-) PIONEER HI-BRED INT INC.
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             92US-00826930.
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Best Local Similarity 100.
Matches 17; Conservative
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                                                                                                   WPI; 1993-236281/30.
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             17-JAN-1992;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAV21968;
                                                                       Grant D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 753
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                                                                                                                                                                                                                                                                                           A (CA)9 simple sequence repeat is used to illustrate the novel method for detecting SSR polymorphisms without the need for direct sequencing or gel electrophoresis. The length of a particular repeat region (i.e. number of repeats) can be highly polymorphic; the sequences flanking the repeat region, however, are conserved. Detection of a SSR of a specific length is achieved by successful ligation of two oligonucleotides, one being exactly complementary to the repeat region and one of its conserved flanking sequences (i.e. comprising the sequence (GT)9) and the other being complementary to the other conserved flanking sequence. (Updated on 10-MAR-2003 to add missing OS field.) (Updated on 25-MAR-2003 to correct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Microsatellite; simple sequence repeat; SSR; polymorphism; variation; genetic marker; human genome; mapping; ligation reaction; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                       Detecting genetic variation between organisms - by detecting polymorphisms in simple sequence repeats in DNA of organisms
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 0.4%; Score 17; DB 1; Length 18; Best Local Similarity 100.0%; Pred. No. 8.6e+02; Matches 17; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 18 BP; 0 A; 0 C; 9 G; 9 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                    Disclosure; Page 5; 8pp; English.
                                                                                                                                (PION-) PIONEER HI-BRED INT INC.
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                                                                        92EP-00311242
                                                                                                      92US-00826930
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/note= "SSR"
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                                                                        09-DEC-1992;
                                                                                                       17-JAN-1992;
               EP552545-A1
                                           28-JUL-1993
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23-DEC-1993
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                                                                                                                                                                 Grant D;
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Gaps

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This antisense oligonucleotide is nuclease resistant and can be used in Ouery Match 0.3%, 7.... No. 8.6 Best Local Similarity 100.0%; Fred. No. 8.6 Claim 4; Col 17-18; 27pp; English Quantitating genetic instability. Basik M; 2335 GTGTGTGTGTGTGTG 2351 BP 18 GIGIGIGIGIGIGIG 2 96US-00734973. 96US-00734973 AAX77462 standard; DNA; 18 (first entry) enhances cellular uptake Anderson G, Stoler D, (HEAL-) HEALTH RES INC. WPI; 1999-357197/30. US5912147 primer 6. 05-AUG-1999 22-OCT-1996; 22-OCT-1996; US5912147-A 15-JUN-1999 Synthetic. AAX77462; RESULT 754 셤

ઠે 염 The treatment of animals, including humans, having a bacterial infection. The treatment of animals, including humans, having a bacterial infection. The treatment comprises administration of such nuclease resistant coligonucleotides, trageted to a nucleic acid or protein of the bacterium, and formulated with a carrier. A compound comprising this nuclease resistant oligonucleotide can be covalently linked to an antibiotic. The method is used to treat infections by a wide variety of Gram-positive and Gram-negative, or acid-fast, bacteria, in human and veterinary medicine. The methods are particularly used in immuno-compromised individuals (e.g. patients with acquired immunodeficiency syndrome or those receiving chemotherapy or radiation therapy), optionally in combination with, or tused to, antiviral or other antimicrobial oligonucleotides. Apart from therapout use, the oligonucleotides can be used to control bacteria in laboratory cultures, foods, beverages and industrial processes. The oligonucleotides are specific for bacteria, without affecting metabolism in mammalian cells. They may also activate RNase H and have a general, on mammalian cells. They may also activate RNase H and have a general, on mammalian calls, intranasally, rectally, topically or by injection, optionally coupled to an agent (e.g. carbohydrate or polyamine) that ö Gaps ö Score 17; DB 1; Length 18; Pred. No. 8.6e+02; 0; Indels Sequence 18 BP; 9 A; 9 C; 0 G; 0 T; 0 U; 0 Other;

Primer, quantitation; genetic instability; tumour cell; detection; neoplastic transformation; carcinogenesis; ss.

This invention describes a novel method for quantitating genetic instability independent of microsatellite alterations by treating a comparison pair comprising genomic DNA from the same including a from normal cells. The method involves the cells from the same individual with oligonucleotide primers selected from (i) a nucleotide sequence (CG)xKG, where R is a purine selected from adenine and guanine and x = 3-7, (ii) a nucleotide sequence (CG)xKY, where R is as in (i) and Y is a pyrimidine selected from cytosine, thymine, and uracil and x = 3-7, (iii)

a nucleotide sequence (CG)xRR, where R is as in (i) and x = 3-7, (iv) a nucleotide sequence (CG)xYY, where Y is a pyrimidine selected from cytosine, thymine, and uracil and x = 3-7, (v) a nucleotide sequence (CA)xRG, where R is a purine selected from adenine and guanine and x = 6-16, (vi) a nucleotide sequence (CA)xRY, where R is a purine selected from adenine and guanine and x = 6-16, where R is a purine selected from adenine and uracil, and x = 6-16, (vii) a nucleotide sequence (CA)xRR, where R is a purine selected from adenine and guanine and x = 6-16, (viii) a nucleotide sequence (CA)xYY, where Y is a pyrimidine selected from cytosine, thymine, and uracil and x = 6-16, and (ix) a combination of the primers. The method is useful for detecting genomic instability which are commonly associated with the various stages of neoplastic transformation and carcinogenesis. The method is rapid and simple 888888888888888888888888

Sequence 18 BP; 8 A; 9 C; 1 G; 0 T; 0 U; 0 Other;

Gaps .. 0 0.4%; Score 17; DB 1; Length 18; 00.0%; Pred. No. 8.6e+02; 0; Indels Query Match 0.4%; Score 17; DB Best Local Similarity 100.0%; Pred. No. 8.6 Matches 17; Conservative 0; Mismatches

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AAX77487 standard; DNA; 18 AAX77487; RESULT 755 AAX77487,

BP

05-AUG-1999 (first entry) USS912147 primer 31.

Primer, quantitation, genetic instability; tumour cell, detection, neoplastic transformation; carcinogenesis; ss.

Synthetic.

US5912147-A

15-JUN-1999

96US-00734973. 22-OCT-1996;

22-OCT-1996;

96US-00734973.

(HEAL-) HEALTH RES INC.

Anderson G, Stoler D,

Basik M;

WPI; 1999-357197/30.

Claim 4; Col 29-30; 27pp; English.

Quantitating genetic instability.

This invention describes a novel method for quantitating genetic instability independent of microsatellite alterations by treating a comparison pair comprising genomic DNA from tumour cells and genomic DNA from normal cells. The method involves the cells from the same individual crom normal cells. The method involves the cells from the same individual with oligonucleotide primers selected from adenine and quantine and x = 3-7 (ii) a nucleotide sequence (CG)xRK, where R is as in (i) and Y is a pyrimidine selected from cytosine, thymine, and uracil and x = 3-7, (iii) anucleotide sequence (CG)xRK, where R is as in (i) and x = 3-7, (iii) anucleotide sequence (CG)xRK, where X is a pyrimidine selected from cytosine, thymine, and uracil and x = 3-7, (v) a nucleotide sequence (CG)xRK, where Y is a pyrimidine selected from cytosine, thymine, and uracil and x = 3-7, (v) a nucleotide sequence (CA)xRK, where R is a purine and guanine and X = 6-16, (vii) a nucleotide sequence (CA)xRK, there R is a purine selected from cytosine, thymine, and uracil, and x = 6-16, (vii) a nucleotide sequence (CA)xRR,

Sequence 18 BP; 8 A; 10 C; 0 G; 0 T; 0 U; 0 Other;

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This invention describes a novel method for quantitating genetic instability independent of microsatellite alterations by treating a comparison genemic DNA from tumour cells and genomic DNA (1i) a nucleotide primers selected from (1) a nucleotide sequence (CG)xXY, where R is as in (i) and x = 3-7, (ii) a nucleotide sequence (CG)xXY, where R is as in (i) and x = 3-7, (iii) a nucleotide sequence (CG)xXY, where R is as in (i) and x = 3-7, (iv) a nucleotide sequence (CG)xXY, where Y is a pyrimidine selected from cytosine, thymine, and uracil and x = 3-7, (v) a nucleotide sequence (CG)xXY, where R is a pyrimidine selected from cytosine, thymine, and uracil and x = 3-7, (vi) a nucleotide sequence (CA)xRY, where R is a purine selected from cytosine, thymine, and uracil, and x = 6-16, (vii) a nucleotide sequence (CA)xXY, where X is a pyrimidine selected from cytosine, thymine, and uracil and x = 6-16, (vii) a nucleotide sequence (CA)xXY, where Y is a pyrimidine selected from cytosine, thymine, and uracil and x = 6-16, (vii) a nucleotide sequence (CA)xXY, where Y is a pyrimidine selected from cytosine, thymine, and uracil and x = 6-16, and (ix) a combination confirment of the primers. The method is useful for detecting genomic instability which are commonly associated with the various stages of neoplastic transformation and carcinogenesis. The method is rapid and simple
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where R is a purine selected from adenine and guanine and x = 6-16, (viii) a nucleotide sequence (CA)xYY, where Y is a pyrimidine selected from cytosine, thymine, and uracil and x = 6-16, and (ix) a combination of the primers. The method is useful for detecting genomic instability which are commonly associated with the various stages of neoplastic transformation and carcinogenesis. The method is rapid and simple
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                                                                                                                                                                                                                                                                                                                                                                                                                   17; Conservative
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This invention describes a novel method for quantitating genetic instability independent of microsatellite alterations by treating a comparison pair comprising genomic DNA from tumour cells and genomic DNA from normal cells. The method involves the cells from the same individual cromparison pair comprising genomic DNA from tumour cells and genomic DNA from normal cells. The method involves the cells from the same individual with oligonucleotide primers selected from define and quanine and x = 3-7 (d); a nucleotide sequence (CG)xRY, where R is as in (i) and X is a pyrimidine selected from cytosine, thymine, and uracil and x = 3-7, (iv) a nucleotide sequence (CG)xRY, where R is a pyrimidine selected from cytosine, thymine, and uracil and x = 3-7, (v) a nucleotide sequence (CA)xRY, where R is a purine selected from dennine and ynanine and x = 6-16, (vi) a nucleotide sequence (CA)xRY, where R is a purine selected from cytosine, thymine, and uracil, and x = 6-16, (vii) a nucleotide sequence (CA)xRY, where R is a purine selected from adenine and guanine and x = 6-16, (vii) a nucleotide sequence (CA)xRY, where R is a pyrimidine selected from cytosine, thymine, and uracil, and x = 6-16, (vii) a nucleotide sequence (CA)xRY, where X is a pyrimidine selected from cytosine, thymine, and uracil and x = 6-16, and (ix) a combination of the primers. The method is useful for detecting genomic instability which are commonly associated with the various stages of neoplastic transformation and carcinogenesis. The method is rapid and simple
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Query Match 0.4%; Score 17; DB 1; Length 18; Best Local Similarity 100.0%; Pred. No. 8.6e+02; Matches 17; Conservative 0; Mismatches 0; Indels
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0.4%; Score 1,; L

Best Local Similarity 100.0%; Pred. No. 8.6

Matches 17; Conservative 0; Mismatches
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2317 CTGTGTGTGTGTGTG 2333

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RESULT 759 AAX77488/c

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Primer, quantitation; genetic instability; tumour cell; detection; neoplastic transformation; carcinogenesis; DNA/RNA hybrid; ss.
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                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                      Claim 4; Col 19-20; 27pp; English
                                                                                                                                                                                                                                         Quantitating genetic instability.
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                                     AAX77464 standard; DNA; 18 BP
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96US-00734973
                                                              (first entry)
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                                                                          US5912147 primer 8.
                                                              05-AUG-1999
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                                                                                                         Synthetic
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misc_RNA
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This invention describes a novel method for quantitating genetic instability independent of microsatellite alterations by treating comparison genomic DNA from tumour cells and genomic DNA from tumour cells and genomic DNA from tumour cells and genomic DNA from tumour cells. The method involves the cells from the same individual with oligonucleotide primers selected from adenine and quantine and x = 3-7 (ii) a nucleotide sequence (CG)xRV, where R is as in (i) and Y is a pyrimidine selected from cytosine, thymine, and uracil and x = 3-7, (iii) a nucleotide sequence (CG)xRY, where R is as in (i) and x = 3-7, (iv) a nucleotide sequence (CG)xRY, where Y is a pyrimidine selected from cytosine, thymine, and uracil and x = 3-7, (v) a nucleotide sequence (CG)xRY, where R is a purine selected from adenine and guantine and x = 6-16, (vi) a nucleotide sequence (CA)xRY, where R is a purine selected from adenine and guantine and x = 6-16, (vii) a nucleotide sequence (CA)xRY, where Y is a pyrimidine selected from cytosine, thymine, and uracil, and x = 6-16, (vii) a nucleotide sequence (CA)xRY, where Y is a pyrimidine selected from cytosine, thymine, and uracil and x = 6-16, and (ix) a combination of the primers. The method is useful for detecting genomic instability which are commonly associated with the various stages of neophastic transformation and carcinogenesis. The method is rapid and simple
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                                     Gaps
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      Score 17; DB 1; Length 18;
Pred. No. 8.6e+02;
                                  0; Indels
0.4%; Scor.
100.0%; Pred. No. e...
... 0; Mismatches
                                                             2317 CTGTGTGTGTGTGTG 2333
        Query Match 0.4
Best Local Similarity 100.
Matches 17; Conservative
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17 CTGTGTGTGTGTGTG 1

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Gaps

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0.4%; Score 17; DB 1; Length 18; 100.0%; Pred. No. 8.6e+02; ive 0; Mismatches 0; Indels

2335 GTGTGTGTGTGTGTG 2351

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Local Similarity 100.

Ouery Match * Best Loca *Matches

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This invention describes a novel method for quantitating genetic instability independent of microsatellite alterations by treating a comparising genomic DNA from themour cells and genomic DNA from themour cells and genomic DNA from themour cells and genomic DNA (COMMAIC), where R is a purine selected from adamine and as = 3-

CCG) xRG, where R is a purine selected from adamine and x = 3-

T, (ii) a nucleotide sequence (CG) xRY, where R is as in (i) and Y is a pyrimidine selected from cytosine, thymine, and uracil and x = 3-7, (iv) a nucleotide sequence (CG) xRY, where R is as in (i) and X = 3-7, (iv) a nucleotide sequence (CG) xRY, where R is a pyrimidine selected from cytosine, thymine, and uracil and x = 3-7, (v) a nucleotide sequence (CG) xRY, where R is a purine selected from adenine and guanine and Y is a pyrimidine selected from cytosine, (vi) a nucleotide sequence (CA) xRY, where R is a purine selected from cytosine, thymine, and uracil, and x = 6-16, (vii) a nucleotide sequence (CA) xRY, where R is a purine selected from cytosine, thymine, and uracil, and x = 6-16, (vii) a nucleotide sequence (CA) xRY, where R is a pyrimidine selected from cytosine, thymine, and uracil and x = 6-16, (vii) a nucleotide sequence (CA) xRY, where X is a pyrimidine selected from cytosine, thymine, and uracil and x = 6-16, and (ix) a combination of the primers The method is useful from decide instability which are commonly associated with the various stages of neoplastic transformation and carcinogenesis. The method is rapid and simple
                                                                                                                                                        Primer; quantitation; genetic instability; tumour cell; detection; neoplastic transformation; carcinogenesis; DNA/RNA hybrid; ss.
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                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 4; Col 29-30; 27pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Quantitating genetic instability.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Basik M;
                                                                                                                                                                                                                                                                                                /*tag= a
/note= "uracil"
AAX77488 standard; DNA; 18 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                       96US-00734973.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              96US-00734973
                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RES INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Anderson G, Stoler D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PI; 1999-357197/30.
                                                                                                                     US5912147 primer 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (HEAL-) HEALTH
                                                                                                                                                                                                                                                                                                                                                                                                                                         22-OCT-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22-OCT-1996;
                                                                              05-AUG-1999
                                                                                                                                                                                                                                                                                                                                                           US5912147-A
                                                                                                                                                                                                                                                                                                                                                                                                  15-JUN-1999
                                                                                                                                                                                                                     Synthetic
                                       AAX77488;
                                                                                                                                                                                                                                                                             misc RNA
                                                                                                                                                                                                                                                             Key
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Sequencing reagent array; primer; capture moiety; hybridisation; detection; mutation; diagnosis; infectious disease; ss.

Sequencing reagent array oligonucleotide primer #28.

used to detect

Reagent for nucleic acid sequencing by primer extension, mutations and to diagnose infectious or genetic diseases

Example 7; Page 27; 47pp; English.

Goelet P, Karn J, Boyce-Jacino M;

WPI; 1999-357855/30

Head SR,

(ORCH-) ORCHID BIOCOMPUTER INC.

97US-00976427. 98WO-US024966

20-NOV-1998; 21-NOV-1997;

WO9927137-A1 03-JUN-1999.

synthetic.

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This invention describes a novel method for quantitating genetic instability independent of microsatellite alterations by treating a comparison pair comprising genomic DNA from tumour cells and genomic DNA from tumour cells and genomic DNA from normal cells. The method involves the cells from the same individual cfrom normal cells. The method involves the cells from the same individual with oligonucleotide primers selected from adenine and guanine and x = 3- (G)xRG, where R is as in (i) and Y is a pyrimidine selected from cytosine, thymine, and uracil and x = 3-7, (ii) a nucleotide sequence (CG)xRY, where R is as in (i) and X = 3-7, (iii) and cytosine, thymine, and uracil and x = 3-7, (v) a nucleotide sequence (CG)xRY, where R is a purine selected from adenine and guanine and x = 6-16, (vii) a nucleotide sequence (CA)xRY, where R is a purine selected from adenine and guanine and x = 6-16, (vii) a nucleotide sequence (CA)xRY, where R is a pyrimidine selected from adenine and guanine selected from cytosine, thymine, and uracil, and x = 6-16, (vii) a nucleotide sequence (CA)xRY, where Y is a pyrimidine selected from cytosine, thymine, and uracil and x = 6-16, (vii) a nucleotide sequence (CA)xRY, where Y is a pyrimidine selected from cytosine, thymine, and uracil and x = 6-16, (vii) a nucleotide sequence (CA)xRY, where X is a pyrimidine selected from cytosine, thymine, and uracil and uracil and x = 6-16, and the primers. The method is useful for detecting genomic instability which are commonly associated with the various stages of neoplastic transformation and carcinogenesis. The method is rapid and simple
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                                                                                                                                                                                                                           Primer, quantitation; genetic instability; tumour cell; detection; neoplastic transformation; carcinogenesis; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 17; DB 1; Length 18;
Pred. No. 8.6e+02;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 18 BP; 8 A; 8 C; 1 G; 1 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Prec.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 4; Col 19-20; 27pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Quantitating genetic instability.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2317 CTGTGTGTGTGTGTG 2333
                                                                                                                                                                                                                                                                                                                                                                                                                                          96US-00734973.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     96US-00734973
                                           AAX77463 standard; DNA; 18
                                                                                                                                    05-AUG-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity 100.
es 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Anderson G, Stoler D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (HEAL-) HEALTH RES INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1999-357197/30
                                                                                                                                                                                    US5912147 primer 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                          22-OCT-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22-OCT-1996;
                                                                                                                                                                                                                                                                                                                                                 US5912147-A
                                                                                                                                                                                                                                                                                                     Synthetic.
                                                                                         AAX77463;
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RESULT 760
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The present invention describes a sequencing reagent (I) comprising: (a) a capture group (GG) that can form a stable complex with a region of a template nucleic acid (II); (b) spacer region (SR); and (c) sequence complex nucleic acid (II). (b) spacer region (SR); and (c) sequence complementary sequence on (II). Also described are: (l) array comprising complementary sequence on (II). Also described are: (l) array comprising (C) method of sequencing (II) using a combinatorial array of (I). Arrays of (I) are used for sequencing nucleic acids by a primer extension complexed. (a) method, e.g. to scan for mutations (particularly single-nucleotide collymorphisms) and for diagnosis of infectious and genetic diseases. Arrays of (I) allow sequencing of templates without any prior knowledge of the wild-type or expected sequence. By separating the capture and specific hybridisation functions, it becomes possible to use smaller primers, simplifying array analysis, reducing costs and allowing cost simplifying array analysis, reducing costs and allowing methods i.e. since primers are required, compared with standard methods i.e. since primer array of n-mers will be as effective as an array of methods i.e. since primers will be as effective length of the primer by 1 base, an array of n-mers will be as effective as an array of n-mers in usual methods. The method may be applied to single or double-stranded by A. Aryofful represent sequencing reagent contains the contains and array of method may be applied to single or double-stranded by A. Aryofful represent sequencing reagent contains and array of method may be applied to single-or double-stranded by A. Aryofful represents sequencing reagent array and allowing array and allowing array and allowing array and allowing array are are described by a pagent array and array of method may be applied to single-or double-stranded by Aryofful represents sequencing reagent array are array are array array are array are array array are array are array array are array array array array array 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                in an example from the present
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100.0%; Pred. No. 8.6e+02;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 18 BP; 0 A; 0 C; 9 G; 9 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     array oligonucleotide primers used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Simple sequence repeat, SSR, #37.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 100.
Matches 17; Conservative
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ID AAS1
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AAX76437 standard; DNA; 18 BP

(first entry)

05-AUG-1999

AAX76437 RESULT 761
AAX76437
ID AAX76437
XX
AC AAX7643

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The invention relates to a substantially purified or isolated nucleic acid (I) from ryegrass or fescue species including a simple sequence crepeat (SSR), having 2 or more tandemly repeated nucleotide core elements 2-6 nucleotides in length. Also included are a nucleic acid primer 2-6 nucleotides in length. Also included are a nucleic acid primer controlled for amplifying an SSR, identifying (M1) an SSR by preparing a clibrary of ryegrass or fescue genomic DNA enriched for SSRs and cidentifying clones in the library containing SSRs, a library of ryegrass or fescue genomic DNA enriched for SSRs prepared by the M1, selecting for a gene in grass or cereal breeding by identifying an SSR that is closely casociated with the gene such that the SSR and the gene are preferentially co-inherited, and selecting for the SSR in the breeding, a cereal for DNA porfiling grass or cereal species varieties by assessing variation between SSR varieties and testing the purity of grass or cereal ceed batches by assessing variation within seed batch of an SSR. The SSRs con profiling grass or cereal species varieties, for testing the purity of grass or cereal section of genes in grass or cereal breeding, for profiling grass or cereal species varieties, for testing the purity of grass or cereal seed batches, and for DNA profiling to establish the contained the contained of the present cereal section of genes or cereal preceding, for distinct identity, uniformity and/or stability of a cultivar. The present
  The invention relates to a substantially purified or isolated nucleic acid (1) from ryegrass or fescue species including a simple sequence repeat (SSR), having 2 or more tandemly repeated nucleotide core elements 2.6 nucleotides in length. Also included are a nucleic acid primer 2.6 nucleotides in length. Also included are a nucleic acid primer continued for amplifying an SSR, identifying (M1) an SSR by preparing a library of ryegrass or feecue genomic DNA enriched for SSRs and cidentifying clones in the library containing SSRs, a library of ryegrass or feecue genomic DNA enriched for SSRs and the W1, selecting for a gene in grass or cereal breeding by identifying an SSR that is closely associated with the gene such that the SSR and the gene are preferentially co-inherited, and selecting for the SSR in the breeding, a method for DNA profiling grass or cereal species varieties by assessing variation between SSR varieties and testing the purity of grass or cereal seed batches by assessing variation within seed batch of an SSR. The SSRs may be used in the selection of genes in grass or cereal breeding, for profiling grass or cereal seed batches, and for DNA profiling to establish the closely distinct identity, uniformity and/or stability of a cultivar. The present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New simple sequence repeats having 2 or more tandemly repeated nucleotide core elements isolated from ryegrass and fescue, useful for selecting of genes in grass or cereal breeding or profiling grass or cereal species
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0.4%; Score 17; DB 1; Length 18; 00.0%; Pred. No. 8.6e+02;
                                                                                                                                                                                                                                                                                       UNIV SOUTHERN CROSS.
STATE VICTORIA DEPT NATURAL RES & ENVIRO.
UNIV ADELAIDE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 18 BP; 0 A; 0 C; 9 G; 9 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                     STATE SOUTH AUSTRALIA SOUTH AUSTRALIAN R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 0.4%; Score 17; DB Best Local Similarity 100.0%; Pred. No. 8.6 Matches 17; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                             (ITMA-) INT MAIZE & WHEAT IMPROVEMENT CENT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sequence is a ryegrass or fescue SSR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 1; Fig 6; 72pp; English.
                                                                                                                                                                                                 24-DEC-1999; 99AU-00004906.
04-MAY-2000; 2000AU-00007310.
                                                                                                                                                       03-JAN-2001; 2001NZ-00509193.
                                                                                                                                                                                                                                                                                                                                                                                                         Forster JW, Jones ES;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-512563/56.
                       Lolium multiflorum.
                                                                                                             25-MAY-2001.
                                                                 NZ509193-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      varieties.
                                                                                                                                                                                                                                                                                              (UYSC-)
(VICT-)
                                                                                                                                                                                                                                                                     (SAUS-)
                                                                                                                                                                                                                                                                                                                                      (UXAD-)
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New simple sequence repeats having 2 or more tandemly repeated nucleotide core elements isolated from ryegrass and fescue, useful for selecting of genes in grass or cereal breeding or profiling grass or cereal species

Claim 6; Page 51; 72pp; English.

varieties.

UNIV SOUTHERN CROSS. STATE VICTORIA DEPT NATURAL RES & ENVIRO. UNIV ADELAIDE. STATE SOUTH AUSTRALIA SOUTH AUSTRALIAN R.

24-DEC-1999; 99AU-00004906. 04-MAY-2000; 2000AU-00007310. 03-JAN-2001; 2001NZ-00509193

SAUS-)

25-MAY-2001 NZ509193-A.

INT MAIZE & WHEAT IMPROVEMENT CENT.

ITMA-) UYAD-) VICT-)

Forster JW, Jones ES; WPI; 2001-512563/56.

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                                                                                                                                                                                                                                                                   Simple sequence repeat; plant; ds; SSR; ryegrass; fescue; tandem repeat; cereal profiling; grass profiling; seed batch purity testing.
                                                  Gaps
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                       Score 17; DB 1; Length 18;
Pred. No. 8.6e+02;
                                                 0; Indels
Sequence 18 BP; 9 A; 9 C; 0 G; 0 T; 0 U; 0 Other;
              0.4%; Scc.,
100.0%; Pred. No. c.
                                                                                                                                                                                                                                             Simple sequence repeat, SSR, #20.
                                                                          2335 GIGIGIGIGIGIGIG 2351
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                                                                                                  17 Grerererererere 1
                                                                                                                                                                 AAS13723 standard; DNA; 18
                                                                                                                                                                                                                    08-MAY-2002 (first entry)
                       Query Match 0.4
Best Local Similarity 100.
Matches 17; Conservative
                                                                                                                                                                                          AAS13723;
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                                                                                                                                        RESULT 764
                                                                                                                                                       AAS13723/c
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Simple sequence repeat; plant; ds; SSR; ryegrass; fescue; tandem repeat; cereal profiling; grass profiling; seed batch purity testing.

Simple sequence repeat, SSR, #29.

(first entry)

08-MAY-2002

XXXXXXXXXXXXXXXX

AAS13732;

AAS13732 standard; DNA; 18 BP

RESULT 763 AAS13732/

g

sequence is a ryegrass or fescue SSR

Gaps ö

0; Indels

2335 GTGTGTGTGTGTGTG 2351 Grerererererere 17 NZ509193-A.

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The invention relates to a substantially purified or isolated nucleic acid (I) from ryegrass or fescue species including a simple sequence crepeat (SSR), having 2 or more tandemly repeated nucleotide core elements 2-6 nucleotides in length. Also included are a nucleic acid primer 2-6 nucleotides or fescue genomic DNA enriched for SSRs and core in the library of ryegrass or fescue genomic DNA enriched for SSRs and included are a nucleic as and core in the library containing SSRs, a library of ryegrass or fescue genomic DNA enriched for SSRs prepared by the MI, selecting for a gene in grass or cereal breeding by identifying an SSR that is closely associated with the gene such that the SSR and the gene are preferentially co-inherited, and selecting for the SSR in the breeding, a method for DNA profiling grass or cereal species varieties by assessing variation between SSR varieties and testing the purity of grass or cereal seed batches by assessing variation within seed batch of an SSR. The SSRs may be used in the selection of genes in grass or cereal breeding, for profiling grass or cereal species varieties for testing the purity of grass or cereal seed batches, and for DNA profiling to establish the content of distinct identity, uniformity and/or stability of a cultivar. The present
                                                                                                                                                                                                                                                                                                                                                                                        New simple sequence repeats having 2 or more tandemly repeated nucleotide core elements isolated from ryegrass and fescue, useful for selecting of genes in grass or cereal breeding or profiling grass or cereal species
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Simple sequence repeat; plant; ds; SSR; ryegrass; fescue; tandem repeat; cereal profiling; grass profiling; seed batch purity testing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0.4%; Score 17; DB 1; Length 18;
100.0%; Pred. No. 8.6e+02;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                         UNIV SOUTHERN CROSS.
STATE VICTORIA DEPT NATURAL RES & ENVIRO.
UNIV ADELAIDE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 18 BP; 9 A; 9 C; 0 G; 0 T; 0 U; 0 Other;
                                                                                                                                                                                             STATE SOUTH AUSTRALIA SOUTH AUSTRALIAN R.
                                                                                                                                                                                                                                                                         INT MAIZE & WHEAT IMPROVEMENT CENT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sequence is a ryegrass or fescue SSR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Simple sequence repeat, SSR, #26.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 6; Page 51; 72pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2335 GTGTGTGTGTGTGT 2351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAS13729 standard; DNA; 18 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18 GIGIGIGIGIGIGIGIG 2
                                                                                              03-JAN-2001; 2001NZ-00509193
                                                                                                                                   24-DEC-1999; 99AU-00004906.
04-MAY-2000; 2000AU-00007310.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17; Conservative
                                                                                                                                                                                                                                                                                                                Forster JW, Jones ES;
                                                                                                                                                                                                                                                                                                                                                       WPI; 2001-512563/56.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       08-MAY-2002
                                                     25-MAY-2001.
                  NZ509193-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         varieties.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAS13729;
                                                                                                                                                                                           (SAUS-) 8
(UYSC-) 1
(VICT-) 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                        (UYAD-)
(ITMA-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
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The invention relates to a substantially purified or isolated nucleic acid (1) from ryegrass or fescue species including a simple sequence repeat (SSR), having 2 or more tandemly repeated nucleotide core elements 2-6 nucleotides in length. Also included are a nucleic acid primer cautable for amplifying an SSR, identifying (M1) an SSR by preparing a library of ryegrass or fescue genomic DNA enriched for SSRs and cannow in the library containing SSRs, a library of ryegrass or fescue genomic DNA enriched for SSRs prepared by the M1, selecting for a gene in grass or cereal breeding by identifying an SSR that is closely associated with the gene such that the SSR and the gene are preferentially co-inherited, and selecting for the SSR in the breeding, a method for DNA profiling grass or cereal species varieties by assessing variation between SSR varieties and testing the purity of grass or cereal species varieties, for profiling grass or cereal species varieties, for profiling grass or cereal species varieties, for testing the purity of grass or cereal species varieties, and for DNA profiling to establish the clisting tidentity, uniformity and/or stability of a cultivar. The present sequence is a ryegrass or fescue SSR
                                                                                                                                                                                                                                                                                                                                                               New simple sequence repeats having 2 or more tandemly repeated nucleotide core elements isolated from ryegrass and fescue, useful for selecting of genes in grass or cereal breeding or profiling grass or cereal species
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Synthetic oligomucleotide; dinucleotide repeat; cytostatic; apoptosis; cell cycle arrest; cell proliferation; caspase; cytokine; interleukin; tumour necrosis factor; TNF; cancer; carcinoma; sarcoma; leukemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0.4%; Score 17; DB 1; Length 18;
00.0%; Pred. No. 8.6e+02;
ve 0; Mismatches 0; Indels
                                                                                                                                                                                          UNIV SOUTHERN CROSS.
STATE VICTORIA DEPT NATURAL RES & ENVIRO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 18 BP; 0 A; 0 C; 9 G; 9 T; 0 U; 0 Other;
                                                                                                                                                                       SAUS-) STATE SOUTH AUSTRALIA SOUTH AUSTRALIAN R.
                                                                                                                                                                                                                                                (ITMA-) INT MAIZE & WHEAT IMPROVEMENT CENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 6; Page 51; 72pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2335 GTGTGTGTGTGTG 2351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ВЪ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 drerererererere 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.08;
                                                                        03-JAN-2001; 2001NZ-00509193.
                                                                                                                                 04-MAY-2000; 2000AU-00007310.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Synthetic oligonucleotide 12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAH46012 standard; DNA; 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 100.
Matches 17; Conservative
                                                                                                                                                                                                                                                                                           Jones ES;
                                                                                                                                                                                                                                  UNIV ADELAIDE
                                                                                                                                                                                                                                                                                                                               WPI; 2001-512563/56.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        lymphoma; ss
                                                                                                                 24-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12-SEP-2001
                                                                                                                                                                                                                                                                                           Forster JW,
                                                                                                                                                                                                                                                                                                                                                                                                                                varieties.
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                                                                                                                                                                                                                (AICT-)
                                                                                                                                                                                              UXSC-)
                                                                                                                                                                                                                                  UYAD-)
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AAH46012
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Synthetic

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The present sequence is that of a synthetic oligonucleotide useful to the invention. The invention relates to a composition, comprising a 2 to 20 base 3'-OH, 5'-OH synthetic oligonucleotide which comprises multiple repeats of dinucleotides such as GT, TG, etc., according to specific formula and having cytostatic activity. The oligonucleotide compositions are useful for inducing cell cycle arrest, inhibition of proliferation, activation of caspases and induction of apoptosis or production of cytokines such as interleukin (IL)-1-beta, IL-6, IL-10, IL-12 and tumour necrosis factor (TNP)-alpha by immune system cells, in an animal having cancer such as primary carcinoma, secondary carcinoma, primary sarcoma and secondary sarcoma such as, leukemia, lymphoma, breast, prostate, colorectal, ovarian or bone cancer. The compositions independent of Fas, p53/p21, p21/waf-1/CIP, p15/ink4B), p16(ink4), drug resistance, caspase 3, transforming growth factor (TGF)-beta 1 receptor
                                                                                                                                                                                                                                                                            Composition comprising synthetic oligonucleotides which comprise multiple repeats of dinucleotides such as GT, TG useful for treating cancer by inducing cell cycle arrest, inhibiting proliferation, activating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Synthetic oligonucleotide; dinucleotide repeat; cytostatic; apoptosis; cell cycle arrest; cell proliferation; caspase; cytokine; interleukin; tumour necrosis factor; TNF; cancer; carcinoma; sarcoma; leukemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0.4%; Score 17; DB 1; Length 18;
.00.0%; Pred. No. 8.6e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 18 BP; 0 A; 0 C; 9 G; 9 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                      Claim 5; Page 17; 77pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2335 GTGTGTGTGTGTGTG 2351
                                                                                                                                                                        (BION-) BIONICHE LIFE SCI INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAH46011 standard; DNA; 18 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.08;
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                                                                                                                     13-DEC-1999; 99US-0170325P.
29-AUG-2000; 2000US-0228925P.
                                                                                    .2-DEC-2000; 2000WO-CA001467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12-DEC-2000; 2000WO-CA001467
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 100.0
Warches 17, Conservative
                                                                                                                                                                                                          Phillips NC, Filion MC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        and hormone dependence
                                                                                                                                                                                                                                             WPI; 2001-398150/42.
                  WO200144465-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200144465-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21-JUN-2001
                                                   21-JUN-2001
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                                                                                                                                                                                                                                                                                                                                       caspases
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AAH46011
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Gaps

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The present sequence is that of a synthetic oligonucleotide useful to the invention. The invention relates to a composition, comprising a 2 to 20 abses 3.-04, 5.-04 synthetic oligonucleotide which comprises multiple repeats of dinucleotides such as GT. TG, etc., according to specific formula and having cytostatic activity. The oligonucleotide compositions are useful for inducing cell cycle arrest, inhibition of proliferation, activation of caspases and induction of apoptosis or production of cytokines such as interleukin (IL)-1. beta, IL-6, IL-10, IL-12 and tumour necrosis factor (INF)-alpha by immune system cells, in an animal having
                                                                                                                                                                        Composition comprising synthetic oligonucleotides which comprise multiple repeats of dinucleotides such as GT, TG useful for treating cancer by inducing cell cycle arrest, inhibiting proliferation, activating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Single nucleotide polymorphism; SNP; single nucleotide primer extension; SNPE; genotyping; agammaglobulinaemia; diabetes insipidus; cancer; Lesch-Nyhan syndrome; muscular dystrophy; familial hypercholesterolaemia; polycystic kidney disease; osteopesis imperfects; autoimmune disease; acute intermittent porphyxia; rheumatoid arthritis; multiple sclerosis; inflammation; forensic investigation; paternity analysis; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cancer such as primary carcinoma, secondary carcinoma, primary sarcoma and secondary sarcoma such as, leukemia, lymphoma, breast, prostate, colorectal, ovarian or bone cancer. The compositions induce apoptosis independent of Fas, p53/p21, p21/waf-1/CIP, p15(ink4B), p16(ink4), drug resistance, caspase 3, transforming growth factor (TGF)-beta 1 receptor and hormone dependence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0.4%; Score 17; DB 1; Length 18; 100.0%; Pred. No. 8.6e+02; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 18 BP; 0 A; 0 C; 9 G; 9 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SNP specific lower PCR primer SEQ ID 310.
                                                                                                                                                                                                                                                                         Claim 5; Page 17; 77pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2335 GTGTGTGTGTGTG 2351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (ORCH-) ORCHID BIOSCIENCES INC
                                                       (BION-) BIONICHE LIFE SCI INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 Grerererererere 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BP
13-DEC-1999; 99US-0170325P.
29-AUG-2000; 2000US-0228925P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13-OCT-2000; 2000WO-US028436.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAH37514 standard; DNA; 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14-AUG-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 100.
Matches 17; Conservative
                                                                                              shillips NC, Filion MC;
                                                                                                                                   WPI; 2001-398150/42.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200129262-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15-OCT-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26-APR-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAH37514;
                                                                                                                                                                                                                                      caspases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 768
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Pohl M;

Picoult-Newburg L,

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Simple Sequence Repeat; SSR; clover; microsatellite; genome mapping;
trait mapping; marker-assisted selection; gene selection; legume;
                                                                                                                                                                                                                                                                                                                                                                                                           (AGRI-) AGRIC VICTORIA SERVICES PTY LTD.
                                                                                                                                                                                                                               2319 GTGTGTGTGTGTGCG 2335
                                                                                                                                                                                                                                       GIGIGIGIGIGIGIGG 17
                                                                                                                                                                                                                                                                                                                                                                               03-JAN-2001; 2001NZ-00509194
                                                                                                                                                                                                                                                                                                                                                                                               2000AU-00006520
                                                                                                                                                                                                                                                                                                                            trait mapping; marker-assis
DNA profiling; breeding; ds
                                                                                                                                                                                                                                                                       AAI64454 standard; DNA; 18
                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                      Koelliker R, Forster JW;
                                                                                                                                                                                                                                                                                                          SSR motif #14.
                                                                                                                                                                                                                                                                                                                                                                                          24-DEC-1999;
28-MAR-2000;
                                                                                                                                                                                                                                                                                              23-NOV-2001
                                                                                                                                                                                                                                                                                                                                             Unidentified
                            acid sample.
                                                                                                                                                                                                                                                                                                                                                                   25-MAY-2001
                                                                                                                                                                                                                                                                                                                                                        NZ509194-A.
                                                                                                                                                                                                                                                                                   AAI64454;
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BP.

99AU-00004907

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The present invention relates to Simple Sequence Repeats (SSRs) from clover species. SSRs, also called microsatellites, are based on a 1-7 mucleotide core element which is trandemly repeated. The SSR array is embedded in complex flanking DNA. SSRs are ideal markers for genome mapping, trait mapping and marker-assisted selection. The SSRs may be used in methods for selecting genes in clover/ legume breeding. The SSRs are also useful for DNA profiling of clover varieties and for testing the purity of legume seed batches. The present sequence is a SSR motif, which was used in the present invention
                                                        Novel simple sequence repeats in clover species useful for selection of genes in legume breeding, for profiling legume species varieties and for testing the purity of legume seed batches.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sheep prion protein microsatellite locus primer #67.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 18 BP; 9 A; 9 C; 0 G; 0 T; 0 U; 0 Other;
                                                                                                                                                                                                       Claim 6; Page 35; 52pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2335 GTGTGTGTGTGTGTG 2351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADO81096 standard; DNA; 18 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17 GTGTGTGTGTGTGTGTG 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 100.
Matches 17; Conservative
WPI; 2001-431058/46.
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                                                                                                                                                                                                                                                                                                                                  suppression (SPRE) primers, and the sequences of regions flanking sites of single nucleotide polymorphisms SNPs. The present invention includes kies for determining the presence or absence of a SNP, using the oligonucleotides of the invention. The PCR primers are used to amplify a coligonucleotides are useful for genotyping a nucleic acid sample by serious as single-nucleotide primer extension reaction. The coligonucleotides are useful for determining the presence, absence or oligonucleotides are useful for determining the presence, absence or identity of a SNP and for genotype of an individual or group of individuals, having a pathological phenotypic trait suspected of being caused by one or more SNPs. Phenotypic traits include diseases e.g. agammaglobulinaemia, diabetes insipidus, besch-nyhan syndrome, muscular dystrophy, familial hypercholesterolaemia, polycystic kidney disease, osteogenesis imperfecta and acute intermittent porphyria. Phenotypic traits also include symptoms of or susceptibility to multifactorial diseases of which a component is or may be genetic such as autoimmune diseases including, rheumatoid arthritis, multiple sclerosis, microorganism. The method is also useful in forensic investigations and microorganism. The present sequence represents a PCR primer specific paternity analysis. The present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                  genotyping oligonucleotide, useful for detecting the presence, ence or identity of single polynucleotide polymorphism in a nucleic
                                                                                                                                                                                                                                                                                                                Sequences AAH37205 - AAH40944 represent PCR primers, single nucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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0
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100.0%; Pred. No. 8.6e+02;
iive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 18 BP; 0 A; 2 C; 9 G; 7 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              for a human SNP containing DNA sequence
                                                                                                                                                                                                                                                 Claim 1; Page 51; 83pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 100.
Matches 17; Conservative
                                      WPI; 2001-290930/30.
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Gaps

; 0

0; Indels

0; Mismatches

100.08;

0.4%; Score 17; DB 1; Length 18; 100.0%; Pred. No. 8.6e+02;

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The invention describes a method of typing (M1) a gene (I) that has one or more polymorphic microsatellite loci (PML). The method comprises: PCR amplification of at least one DNA region of (I) that includes PML, using as template a DNA sample containing at least one segment of (I); and determining the length of the resulting amplicon(s). Also described are: a method of determining (M2) microsatellite markers (MM) for
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Typing genes that contain polymorphic microsatellite loci, useful for identifying predisposition to disease, by amplification and determining length of amplicons.
                                                                                                     gene typing; polymorphic microsatellite loci; PML; disease; disease predisposition; microsatellite marker; prion disease; cystic fibrosis; malignant hyperthermia syndrome; metabolic disease; milk protein; hormone; transcription factor; pT7-blue-vector; sheep;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 3; Page 30; 64pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                   Han Y;
                                                                                                                                                                          microsatellite; PCR; primer; ss
                                                                                                                                                                                                                                                                                                      09-AUG-2002; 2002DE-01036711.
                                                                                                                                                                                                                                                                                                                                    09-AUG-2002; 2002DE-01036711.
                                                                                                                                                                                                                                                                                                                                                                                                   Preuss S,
                                                                                                                                                                                                                                                                                                                                                                  (UYHO-) UNIV HOHENHEIM
                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2004-215730/21.
                                                                                                                                                                                                                                                                                                                                                                                                  Geldermann H,
                                                                                                                                                                                                                                      DE10236711-A1
                                                                                                                                                                                                                                                                        26-FEB-2004.
                                                                                                                                                                                                          Ovis aries
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more PML; and prediagnosis (M3) of diseases associated with gene that include PML. The method is used to identify microsatellite markers, in a disease-related gene, that are associated with a predisposition to diseases and for prediagnosis of such diseases, especially prion diseases but also cystic fibrosis, malignant hyperthermia syndrome in pigs and metabolic diseases; also to type genes that encode milk proteins, hormones or transcription factors. The method is simpler, quicker and particularly less expensive than known methods based on sequencing. This sequence represents a primer used to genotype a region of the sheep prion protein (PrP) comprising a polymorphic microsatellite locus. predisposition to a disease, associated with a gene that includes one or 8866666666666688888

Sequence 18 BP; 9 A; 9 C; 0 G; 0 T; 0 U; 0 Other;

0.4%; Score 17; DB 1; Length 18; 100.0%; Pred. No. 8.6e+02; Indels ö 100.0%; Pred. 2335 GTGTGTGTGTGTGTG 2351 17 GTGTGTGTGTGTGTG 1 17; Conservative Local Similarity Query Match Matches ઠે

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ADI80140 standard; DNA; 20 BP

(first entry) 22-APR-2004 ADI80140;

Mouse transforming growth factor-beta 2 antisense oligo, SEQ ID No 141.

antisense; transforming growth factor; TGF; beta 2; TGF-beta 2; cytostatic; nootropic; neuroprotective; immunosuppressive; hyperproliferative disorder; cancer; neurodegenerative; hyperactivation; immune, ss; mouse; murine

Mus musculus

US2004006030-A1

08-JAN-2004

02-JUL-2002; 2002US-00189267.

02-JUL-2002; 2002US-00189267.

(ISIS-) ISIS PHARM INC

Dobie KW Monia BP, Freier SM,

WPI; 2004-081742/08.

New compounds, particularly antisense oligonucleotides targeted to a nucleic acid encoding TGF-beta 2, useful for treating cancer, a neurodegenerative disorder, or a disease involving hyperactivation of immune response

Example 16; SEQ ID NO 141; 135pp; English.

The invention relates to a novel antisense compound of 8-80 nucleobases in length targeted to, and which specifically hybridizes with, a nucleic acid molecule encoding transforming growth factor (TGF) beta 2, and inhibits the expression of TGF-beta 2. The invention further relates to a compound 8-80 nucleobase in length that specifically hybridizes with at least an 8-nucleobase portion of an active site on a nucleic acid molecule encoding TGF-beta 2, a composition comprising the compound and carrier or diluent, inhibiting the expression of TGF-beta 2 in cells or tissues by contacting the cells or tissues with the compound so that expression of TGF-beta 2 is inhibited; treating an animal having a disease or condition associated with TGF-beta 2 by administering to the animal a therapeutic or prophylactic amount of the compound so that

expression of TGF-beta 2 is inhibited, and screening an antisense compound. The antisense compound has cytostatic, nootropic, neuroprotective, and immunosuppressive activities. The compound composition and methods are useful for treating a disease or condition associated with TGF-beta 2, such as a hyperproliferative disorder e.g. cancer, a neurodegenerative disorder, or a disease or condition involving hyperactivation of an immune response. This polynucleotide sequence hyperactivation of an immune response. This polynucleotide sequence represents an antisense oligonucleotide of the invention. 8\$666666688888

Sequence 20 BP; 6 A; 6 C; 6 G; 2 T; 0 U; 0 Other;

Gaps ö DB 1; Length 20; 9.7e+02; 0; Indels 0.4%; brod. No. .. 100.0%; Pred. No. .. Query Match Best Local Similarity 100.' Matches 17; Conservative

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3393 3377 TIGCIGIGIGICCCAGG 18 rrecrerererereceaes ò 셤

Gaps

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RESULT 772 ADI80261

ADI80261 standard; DNA; 20

BP

ADI80261;

(first entry) 22-APR-2004 antisense; transforming growth factor; TGF; beta 2; TGF-beta 2; cytostatic; nootropic; neuroprotective; immunosuppressive; hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;

Mouse transforming growth factor-beta 2 target DNA region, SEQ ID No 262.

mmune; ss; mouse; murine.

Mus musculus.

US2004006030-A1.

08-JAN-2004.

02-JUL-2002; 2002US-00189267

02-JUL-2002; 2002US-00189267

(ISIS-) ISIS PHARM INC

Dobie KW; Freier SM, Monia BP,

WPI; 2004-081742/08

New compounds, particularly antisense oligonucleotides targeted to a nucleic acid encoding TGF-beta 2, useful for treating cancer, a neurodegenerative disorder, or a disease involving hyperactivation of immune response.

Example 16; SEQ ID NO 262; 135pp; English.

The invention relates to a novel antisense compound of 8-80 nucleobases in length targeted to, and which specifically hybridizes with, a nucleic acid molecule encoding transforming growth factor (TGF)-beta 2, and inhibits the expression of TGF-beta 2. The invention further relates to:

a compound 8-80 nucleobase prior of an active site on a nucleic acid at least an 8-nucleobase portion of an active site on a nucleic acid molecule encoding TGF-beta 2; a composition comprising the compound and a carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or tissues by contacting the cells or tissues with the compound so that expression of TGF-beta 2 is inhibited; treating an animal having a disease or condition associated with TGF-beta 2 by administering to the animal a therapeutic or prophylactic amount of the compound so that animal a therapeutic or prophylactic amount of the compound so that compound. The antisense compound has cytostatic, nootropic, neuroprotective, and immunosuppressive activities. The compound,

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composition and methods are useful for treating a disease or condition associated with TGF-beta 2, such as a hyperproliferative disorder e.g. cancer, a meurodegenerative disorder, or a disease or condition involving hyperactivation of an immune response. This polynucleotide sequence represents a preferred target DNA region of TGF-beta 2 of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            chimeric; antisense oligonucleotide; phosphorothioate; human; microsomal prostaglandin E2 synthase; mPGES-1; mPGES-1; inhibitor; microsomal prostaglandin E2 synthase; inhibitor; cytostatic; antidiabetic; immunomodulator; cardiant; neuroprotective; antiinflammatory; neuroprotective; antiarthritic; vasotropic; ophthalmological; immunomodulatory; cardiavascular; gene therapy; inflammation; Alzheimer's disease; arthritis; diabetes; cancer; ischaemia; reperfusion injury; ophthalmic disorder; immunological disorder; cardiovascular disorder; neurological disorder; se.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New antisense compound, having a sequence targeted to a nucleic acid encoding mPGES-1, useful for preparing a composition for treating e.g., inflammation, Alzheimer's disease, arthritis, diabetes, cancer or ischemia.
                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human mPGES-1 chimeric antisense oligonucleotide SEQ ID NO:1191.
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                                                                                                                                                                                                                                                 Score 17; DB 1; Length 20;
Pred. No. 9.7e+02;
                                                                                                                                                                                       Sequence 20 BP; 2 A; 6 C; 6 G; 6 T; 0 U; 0 Other;
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/mod_base= OTHER
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16. .20
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/mod_base= OTHER
/note= "2'-O-methoxyethyls"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADM15004 standard; DNA; 20 BP
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                                                                                                                                                                                                                                                    0.48;
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es 17; Conservative
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Matches
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ADM15004/c
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thuman mPGES-1 gene is located on chromosome 9, more specifically to gad 4.3. The present invention also describes: (1) antisense compounds, baving a sequence comprising 8-30 bp targeted to a nucleic acid encoding mPGES-1, which specifically hybridise with the nucleic acid mPGES-1 and inhibits its expression; (2) a method of inhibiting the expression of mPGES-1 in cells or tissues; and (3) a method of treating an animal condition associated with mPGES-1. MPGES-1 chimeric antidiabetic, immunomodulator, cardiant, neuroprotective, antidiamatory, neuroprotective, nootropic, antistnession; (2) antihibitors and an gardiant, neuroprotective, associated, immunomodulatory and cardiovascular activities, and can be used as mPGES-1 inhibitors and in gene therapy. The antisense compound condition associated with mPGES-1, infimmation, Alzheimer's dispase, arthibite dishers and in gene therapy. The antisense compound condition associated with mPGES-1 e. infimmation, Alzheimer's
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                                                                                                                                                                                                                                                                                                                                                                         disease, arthritis, diabetes, cancer, ischaemia or reperfusion injury, or ophthalmic, immunological, cardiovascular or neurological disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             numan; ss; primer; calcitonin receptor-like receptor; CRLR; hypertension; glucocorticoid administration; tumour; vasodilation; anglogenesis; gene therapy; PCR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Use of calcitonin receptor-like receptor (CRLR) genes for determining if a test compound can regulate expression of CRLR gene, for screening a test compound to counteract hypertension in glucocorticoid administration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to the use of the calcitonin receptor-like receptor (CRLR) gene for determining whether a test compound can regulate expression of CRLR gene, screening a test compound for ability to
                                                     The present sequence represents a chimeric antisense oligonucleotide targeted to human microsomal prostaglandin E2 synthase (mPGES-1). The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0.4%; Score 17; DB 1; Length 20; 00.0%; Pred. No. 9.7e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 20 BP; 11 A; 9 C; 0 G; 0 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human CRLR gene 5' flanking region PCR primer #2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Prec. ...
                  Claim 4; SEQ ID NO 1191; 132pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rees CMP, Nikitenko LL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 4; Page 24; 43pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
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counteract hypertension in the course of glucocorticoid administration to a patient, diagnosing a lesion as a tumour reducing the hypertensive of aide effect of a glucocorticoid administration regime in a patient, or for tumour therapy. The agents, e.g. adrenomedullin, CGRP or functional analogues of the peptides are useful in manufacture of a preparation for reducing the hypertensive side effect of a glucocorticoid administration regime. The compound that up-regulates CRLM gene expression or the up-regulator of CRLM gene promoter activity is also useful in the up-regulator of a preparation for reducing the hypertensive side-effect of a glucocorticoid administration regime or for treating a condition where it is desired to promote vasodilation and/or angiogenesis. The compound that up-regulates CRLM expression in microvascular endothelial cells under hypoxic conditions is useful in the manufacture of a medicament for use in tumour therapy, e.g. a patient identified as having a tumour constitute of a combined preparation for simultaneous, sequential or combined administration of the compound with an analogue is useful in the manufacture of a preparation for up-regulating the CRLM or elevated Corresponding mMNA. It is a also care an analogue is useful in the manufacture of a preparation for up-regulating the CRLM gene promoter in micro vascular endothelial cells or cragulating the CRLM gene promoter in micro vascular endothelial cells or corresponding mNA in the manufacture of a preparation for up-capulating a glucocorticoid responsive promoter derived from a cRLM gene in a vector administered for gene therapy. The compound capulating a glucocorticoid responsive promoter derived from a crientified as an up-regulator of CRLM gene in up-regulating responsive promoter derived from a crientified as an up-regulator of CRLM gene in up-regulating responsive promoter derived from a crientified as an up-regulation of the compound and a vector administered for gene therapy. The compounce in a vector administered for gene p
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Sequence 20 BP; 8 A; 10 C; 1 G; 1 T; 0 U; 0 Other;

Query Match 0.4%; Score 17; DB 1; Length 20; Best Local Similarity 100.0%; Pred. No. 9.7e+02; Matches 17; Conservative 0; Mismatches 0; Indels 2333 GCGTGTGTGTGTGTG 2349 17 GCGTGTGTGTGTGTGTG ઠે 셤

ADP45829 standard; DNA; 20 BP ADP45829;

26-AUG-2004 (first entry)

Extend primer 21 used to genotype human ICAM-1/ICAM-4/ICAM-5 SNP

breast cancer; cytostatic; gene therapy; human; intercellular adhesion molecule; ICAM-1; human rhinovirus receptor; BB2; CD54; cell surface glycoprotein P3.58; ICAM-4; Landsteiner Wiener blood group; ICAM-5; telencephalin; chromosome 19p13; ss; primer; PCR; SNP; single nucleotide polymorphism; probe.

Homo sapiens.

WO2004047623-A2

LO-JUN-2004.

25-NOV-2003; 2003WO-US037948

25-NOV-2002; 2002US-0429136P. 24-JUL-2003; 2003US-0490234P.

(SEQU-) SEQUENOM INC.

Reneland R; Kammerer SM, Braun A, Roth RB, Nelson MR,

WPI; 2004-441051/41

ö The invention relates to a novel method for identifying a subject at risk of breast cancer comprising detecting the presence or absence of one or more polymorphic variations associated with breast cancer in a nucleic acid sample from a subject. The method of the invention has cytostatic applications and may be useful for identifying a subject at risk of breast cancer, for early diagnosis, prevention and treatment of breast cancer, possibly via gene therapy, as well as to analyse and predict a response to a breast cancer treatment and in clinical drug trials. The current sequence is that of an Extend primer (also described as probe) of the invention which was used to genotype human intercellular adhesion molecule ICAM-1/ICAM-4/ICAM-5 gDNA. ICAM-1 (human rhinovirus receptor; BB2 postition 19p13.2-p13.2, ICAM-4 (Landsteiner-Wiener blood group; LW) has been mapped to chromosomal position 19p13.2-cen and ICAM-5 Identifying a subject at risk of breast cancer by detecting the presence of polymorphic variations in the ICAM, MAPKIO, KIAA0861, NUMA1 or GALE regions which are associated with breast cancer in a nucleic acid sample Gaps telencephalin) has been mapped to chromosomal position 19p13.2. ; 0 Score 17; DB 1; Length 20; Pred. No. 9.7e+02; 0; Indels Sequence 20 BP; 1 A; 1 C; 10 G; 8 T; 0 U; 0 Other; 0.4%; bcc_ 100.0%; Pred No. ... 0; Mismatches Example 4; Page 83; 289pp; English 2329 GTGTGCGTGTGTGTG 2345 4 Grerecerererere 20 Best Local Similarity 100. Matches 17; Conservative from a subject. Query Match ò 셤

AAQ34146 standard; DNA; 23 BP RESULT 776 AAQ34146

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Gaps

; 0

(revised)
(first entry) 25-MAR-2003 02-FEB-1993 AAQ34146;

Sequence of a microsatellite from clone TGLA77.

PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage; genetic mapping; traits; amplification; ss.

Bos taurus.

WO9213102-A1,

06-AUG-1992.

92WO-US000340. 15-JAN-1992;

91US-00642342. .S-JAN-1991;

(GENM-) GENMARK.

Georges M, Massey JM;

WPI; 1992-284684/34.

Polymorphic bovine DNA markers - used in genetic identification, gene mapping, and selective breeding.

Table 7; Page 389; 517pp; English.

The sequence is that of a bovine microsatellite sequence obtd. by screening a library of bovine MboI DNA fragments of between 250 and 500 bp with an (AC)15 and a (TC)15 oligonucleotide probe. One out of 50 clones cross-hybridised. Assuming independent distribution of

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Gaps

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> Mismatches

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17; Conservative

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Matches
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                   in the bovine genome is estimated at >100, 000. The sequence information for ca. 230 such bovine microsatellites is summarised in the seperation and indexed herein (see below). The sequences upstream and downstream of the microsatellite sequence were used to generate the required PCR primers for in vitro amplification of the corresp. microsatellite (using the program OPTIRRIM). The microsatellites may be used to identify individuals, for parentage testing, and in the genetic mapping of economic trait loci, or genes involved the determinism of economically important traits esp. in cattle, to allow selective breeding. See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN
  microsatellites and MboI sites, the frequency of (T6)n >9 microsatellites
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human papilloma virus; HPV; HPV16; HPV18; diagnosis; primer;
capture probe; hybridization; self-sustained sequence replication; 3SR;
E6 protein; E7 protein; cervical dysplasia; cervix cancer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human papilloma virus detection assay - by amplification using self sustained sequence replication and hybridisation with a detector probe.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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0
                                                                                                                                                                                                                                                                                                                                                                                              Length 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
                                                                                                                                                                                                                                                                                                                                                Sequence 23 BP; 0 A; 0 C; 12 G; 11 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Seguence 24 BP; 9 A; 5 C; 7 G; 3 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                              0.4%; Score 17; DB 1; L. 100.0%; Pred. No. 1.1e+03; ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 16; 79pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2335 GIGIGIGIGIGIGIGIG 2351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (BAXT ) BAXTER DIAGNOSTICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAQ75505 standard; DNA; 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                     17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Capture probe CAP267.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1995-006821/01.
                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO9426934-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25-MAR-2003
28-JUN-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAQ75505;
                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                            field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Jatches
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AAQ75505/
  8 \times 9 
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0.4%; Score 17; DB 1; Length 24; 100.0%; Pred. No. 1.2e+03;

Best Local Similarity

Query Match

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cloning and expression of PUR protein, involved in regulation of DNA replication - also oligo:nucleotide(s) and antibodies for use in the treatment of proliferative diseases, e.g. cancer.
                                                                                                                                                                                                                                                                                                                                                                                    Single-strand binding protein; PUR protein; cellular oncogene; eukaryotic origin of replication; gene amplification; cancer cell; retinoblastoma protein; helix-destabilising protein; inhibitor; hyperproliferation; c-myc; rapid amplification of cDNA ends; ss.
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Pred. No. 1e+03;
0; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 1; Page 11; 97pp; English
                                                                                                                                                                                                                                                                                                                                                Pur-specific RACE primer EX-990.
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2988 TTTTTCTGCCACCCCAG 3004
                                                                                                                                                                      BP.
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93US-00014943.
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Best Local Similarity 90.0%;
Matches 18; Conservative
                                              21 TTTTTCTGGCACCGCAG
                                                                                                                                                                      AAQ44813 standard; DNA; 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAX59720 standard; DNA; 20
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28-SEP-1994
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Synthetic.
                                                                                                                                                                                                                          AAQ44813;
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                                                                                                                           RESULT 778
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Oligodeoxyribonucleotide; intersubunit linkage;
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                                                                                                                                                                                                                                                                                                                                 94US-00210505.
94US-00214599.
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                                                                  qenetic disorder; cancer; ss
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les 18; Conservative
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                                                                                                                                Key
modified_base
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                                                                                                                                                                                                                                                                                                  20-MAR-1995;
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                                                                                                                                                                                                                                                                                                                                                   18-MAR-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RNA strands.
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                                                                                                                                                                                                                                                                   28-SEP-1995
                                                                                                 Synthetic
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 oligodeoxyribonuclectides are more resistant to nuclease digestion and have improved RNA and dsDNA hybridisation characteristics, relative to oligonucleotides not containing N3'-P5' phosphoramidate linkages. They also have excellent antisense activity against complementary mRNA targets in in-vitro cell growth inhibition assays. They also exhibit low cytotoxicity. They may be used in diagnostic and therapeutic applications, e.g., in combatting infections agents such as bacteria, viruses, etc. or in treatment of smooth muscle cell proliferation disorders, inflammatory processes, certain genetic disorders, cancers, etc. . The present sequence represents an oligonucleotide of the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The specification describes oligodeoxyribonucleotides having contiguous nucleoside subunits joined by intersubunit linkages, where at least 3 contiguous subunits are joined by phosphoramidate intersubunits. The oligodeoxyribonucleotides has a sequence of nucleoside subunits effective to form a duplex with a target nucleic acid molecule. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Oligo:nucleotide N3'-P5' phosphoramidate(s) - have improved resistance toward phosphodiesterase digestion, and form stable duplexes with DNA and
                                                                                                                                                                             /*tag= a
/note= "each base is linked by N3'-P5' phosphoramidate
linkages"
                               phosphoramidate intersubunit; antisense activity; nuclease resistant; in-vitro cell growth inhibition assay; infection; smooth muscle cell proliferation disorder; inflammatory process;
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                 intersubunit linkage;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Page 55; 101pp; English
                                                                                                                                                Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Chen J;
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                                                                                 genetic disorder; cancer; ss.
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                                                                                                                                                                                                                                                                                                                   95WO-US003575
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                 Oligodeoxyribonucleotide;
                                                                                                                                                                                                                                                                                                                                                                                                                                    Schultz RG,
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nes 18; Conservative
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                                                                                                                                                                                                                                                                                                                                                    18-MAR-1994;
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                                                                                                                 Synthetic
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disorders, inflammatory processes, certain genetic disorders, cancers, etc. . The present sequence represents an oligonucleotide of the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    /*tag= a
/note= "each base is linked by N3'-P5' phosphoramidate
phosphoramidate intersubunit; antisense activity; nuclease resistant; in-vitro cell growth inhibition assay; infection; smooth muscle cell proliferation disorder; inflammatory process;
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Gaps

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0.4%; Score 16.8; DB 1; Length 20; 90.0%; Pred. No. 1e+03; ive 0; Mismatches 2; Indels

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The primers AAT99265-T99269 were used to PCR amplify and isolate the complete sequence of the human PUR-alpha gene (AAT99264). This primer corresponds to nucleotides 990-1009 of the PUR sequence. The PUR sequence can be used to identify chemical or biological compounds that bind to PUR or binding fragments of PUR. Inhibitors of PUR activity may be used to
                                                      PUR protein ligands or modulators - using immobilised PUR fragments, to treat hyper-proliferative diseases, e.g. cancer.
                                                                                                                                                                                                       Sequence 20 BP; 9 A; 8 C; 1 G; 2 T; 0 U; 0 Other;
                                                                                                                                                                               treat hyperproliferative diseases such as cancer
                                                                                                                                                                                                                                                                              2329 GIGIGGGIGIGIGIGI 2348
                                                                                             Disclosure; Col 9; 64pp; English.
           Johnson EM;
                                                                                                                                                                                                                               Query Match 0.4
Best Local Similarity 90.0
Matches 18; Conservative
                                   WPI; 1997-488859/45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bergemann AD,
           Bergemann AD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28-AUG-1992;
02-FEB-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     36-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                               24-SEP-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US5756684-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26-MAY-1998
                                                          Assays for
protein or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Synthetic
                                                                                                                                                                                                                                                                                                                                                                                         AAV31725;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                           RESULT 783
                                                                                                                                                                                                                                                                                                                                                       AAV31725/
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                                                                                                                                                                                                                                                                                                   The present sequence represents a specifically claimed oligonucleotide PCR primer. The oligonucleotide can be used for polymerase chain reaction (PCR) amplification of DNA, specifically regions of specific genes that are conserved among mammalian species, i.e. pairs of oligonucleotides from the present specification represent universal mammalian sequence-tagged site (UM-STS) primers. The primers are used to develop genomic maps, to isolate clones from libraries, to make cross-species comparisons and to develop additional genetic markers. UM-STS allow genomic comparisons to be made between more species
                                                                                                                                                                                                                                New oligonucleotide primers amplifying gene regions conserved among mammals - useful for developing genomic maps, isolating clones and making cross-species comparisons.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 human; c-myc; inhibitor; hyperproliferative disease; ss; primer; amplification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
 universal mammalian sequence tagged site; genomic map; clone; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                  0.4%; Score 16.8; DB 1; Length 20; 90.0%; Pred. No. 1e+03; ive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 20 BP; 4 A; 5 C; 7 G; 4 T; 0 U; 0 Other;
                                                                                                                                                                                  Yuzbasiyan-Gurkan V;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SINAI SCHOOL MEDICINE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human PUR-alpha gene primer EX-990.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1744 CCCGTGAAGTGGATGGCGCC 1763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ccrereaagregaregeacc 20
                                                                                                                                                                                                                                                                                 Claim 1; Page 9; 26pp; English.
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93US-00014943.
95US-00470911.
                                                                                                97WO-US002403
                                                                                                                        96US-0012061P
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                                                                                                                                             (UNMI ) UNIV MICHIGAN.
(UNMS ) UNIV MICHIGAN STATE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAT99269 standard; DNA;
                                                                                                                                                                                   Brewer GJ, Venta PJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PUR element; human;
cancer; PCR; primer;
                                                                                                                                                                                                       WPI; 1997-435083/40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
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                                                                                                18-FEB-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
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                                                 WO9731012-A1
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02-FEB-1993;
                                                                        28-AUG-1997
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                         Synthetic
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Matches
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This is the nucleotide sequence of the PUR psecific PCR primer used for amplification in the method of the invention, involving the use of the PUR protein and its fragments, which inhibit PUR protein binding to PUR element or other proteins. Inhibitors of PUR activity may be useful for treating viral infections and hyperproliferative diseases such as cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PUR protein and its fragments - that inhibit PUR protein binding to PUR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PUR-alpha gene; inhibition; viral infection; cancer; PCR; primer; hyperproliferative disease; amplification; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0.4%; Score 16.8; DB 1; Length 20;
                                                                                                                                                                                                                                                                                                                                                                                                    Nucleotide sequence of the PUR specific PCR primer Ex-990.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 20 BP; 9 A; 8 C; 1 G; 2 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (MOUN ) MOUNT SINAI SCHOOL MEDICINE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Col 9; 63pp; English.
20 Grardcardrardrardr 1
                                                                                                                                                                                 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           95US-00470911.
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                                                                                                                                                                                 AAV31725 standard; DNA; 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Johnson EM;
                                                                                                                                                                                                                                                                                                                            (first entry)
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Matches

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The invention provides a novel method for isolation of satellite sequences from genomic DNA that comprises fragmentation of the DNA by a method which is not dependent on base sequences, then selection of the satellite sequences from the obtained genomic library of high homogeneity. The method is useful for the isolation of microsatellite DNA sequences which can be used as DNA markers. The new method markedly improves the efficiency of isolation of satellite sequences in comparison to prior art methods which are reliant on base sequences. Sequences AAZ98483-514 represent sequences from Haliotis discus, used in the method
                                                                                                                                                                                                                                                                                                                                                         Isolation of satellite sequences from genomic DNA for use as DNA markers comprises isolating a library with high homogeneity by DNA fragmentation.
                sequence; DNA fragmentation; microsatellite DNA; DNA marker;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rat; Nurr1; tyrosine hydroxylase; catecholamine-related disease;
Parkinson's disease; manic depression; schizophrenia; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 16.8; DB 1; Length 20;
Pred. No. 1e+03;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 20 BP; 11 A; 9 C; 0 G; 0 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                    (NORQ ) JAPAN MIN AGRIC FORESTRY & FISHERIES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rat FGFR coding sequence PCR primer #2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (SALK ) SALK INST BIOLOGICAL STUDIES.
                                                                                                                                                                                                                                                                                                                                                                                                                 Example 5; Page 14; 35pp; Japanese.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sakurada K, Palmer T, Gage FH;
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                                                                                                                                                                                                               98JP-00232153
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                                                                                                                                                                                                                                                                                        Sekino M;
                                                                                                                                                                                                                                                                                                                         WPI; 2000-224692/19.
                  Satellite sequence;
Haliotis discus; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rattus norvegicus.
                                                                      Haliotis discus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200058451-A1.
                                                                                                        WO200011156-A1
                                                                                                                                                                               01-JUL-1999;
                                                                                                                                                                                                                  18-AUG-1998;
                                                                                                                                                                                                                                                                                        Takahashi H,
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                                                                                                                                            02-MAR-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention describes a monoclonal antibody that specifically binds to an epitope of the PUR protein. Antibodies that bind to the PUR protein and neutralise PUR activity may be used to treat hyperproliferative diseases such as cancer. PUR antibodies may be used diagnostically to detect aberrant expression of the PUR protein and/or mutations in the PUR gene. The present sequence represents a PUR-lipha RACE primer which is used in an example from the present invention
                                                                                                                                                                                                                                                                                                                         PUR element; PUR-alpha; hyperproliferative disease; cancer; human; monoclonal antibody; identification; characterisation; RACE primer; ss.
                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Monoclonal antibody specific for PUR protein - useful for treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
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Pred. No. 1e+03;
0; Mismatches 2; Indels
                  2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 20 BP; 9 A; 8 C; 1 G; 2 T; 0 U; 0 Other;
 Pred. No. 1e+03;
                  0; Mismatches
                                                                                                                                                                                                                                                                                         PUR-alpha RACE reaction primer EX-990.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2329 GIGIGGGIGIGIGIGI 2348
                                                      'GTGT 2348
                                                                                       20 Grardcardrardrardr
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                                                                                                                                                                               AAX04091 standard; DNA; 20 BP
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93US-00014943.
95US-00470911.
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90.06;
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                  18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity 90.0 es 18; Conservative
                                                      2329 GTGTGCGTGTGTGTGTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1999-152881/13.
 Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17-JUN-1995;
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02-FEB-1993;
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                                                                                                                                                                                                                                                                                                                                                                                 Synthetic
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RESULT 78, AAXO, 091/AXO, 001/AXO, 001/

RESULT 785

AAZ98503

8X4X5X8

Matches

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Gaps

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Seguence 20 BP; 5 A; 6 C; 2 G; 5 T; 0 U; 2 Other;
                                                                                                                                                 1666 ATGAAGATCGCAGACTTCGG 1685
                                        Example 1; Page 20; 68pp; English
                                                                                                                                                                                                                                                                                                                                                                  inflammation or tumor formation.
                                                                                                                                                        20 ATGAAGATHGCDGACTTTGG 1
                                                                                                                                                                                                                                                                                                                                                                              Claim 1; Col 43; 40pp; English.
                                                                                                                                                                                         AAF91351 standard; DNA; 20 BP
                                                                                                                                                                                                                                                                                            02-MAR-2000; 2000US-00517584
                                                                                                                                                                                                                                                                                                        02-MAR-2000; 2000US-00517584
                                                                                                                                                                                                                (first entry)
                                                                                                                                     17; Conservative
                                                                                                                                                                                                                                                                                                                               Brown-Driver
                                                                                                                                                                                                                                                                                                                    (ISIS-) ISIS PHARM INC
                                                                                                                                                                                                                                                                                                                                          WPI; 2001-190981/19.
     WPI; 2000-656165/63.
                                                                                                                               Best Local Similarity
                                                                                                                                                                                                                                                          Homo sapiens.
                                                                                                                                                                                                                                                                     US6187587-B1,
                                                                                                                                                                                                                04-MAY-2001
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                                                                                                                                                                                                     AAF91351;
                                                                                                                         Query Match
                                                                                                                                                                              Matches
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Cowsert LM;

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2; Mismatches

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New antisense compound targeted to a region of a nucleic acid encoding human Integrin beta 4 binding protein and that inhibits expression of the nucleic acid, for treating e.g. cancer.
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                                                                                                                                                                                                                                                                                                                                                  Antisense; human Integrin beta 4 binding protein; hIbeta4BP; cytostatic; cell proliferation; cancer; gene therapy; phosphorothioate backbone; ss.
                                    Gaps
                                    .
0
Length 20;
                                    Indels
                                                                                                                                                                                                                                                                                                               Human hibeta4BP antisense oligonucleotide, ISIS #129427
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/mod_base= OTHER
/note= "2'methoxyethyl nucleotides"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           note = "2'methoxyethyl nucleotides"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'note = "Phosphorothioate backbone"
0.4%; Score 16.8; DB 1;
90.0%; Pred. No. 1e+03;
iive 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                          2325 GTGTGTGTGCGTGTGTGTGT 2344
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/*tag= a
/mod_base= OTHER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'mod_base= OTHER
                                                                                                 20 GTGTGTGAGCATGTGTGT 1
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/mod_base= m5c
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AAD35726 standard; DNA; 20
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                   Best Local Similarity
Matches 18; Conserv
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modified_base
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                                                                                                                                                                                                                                                                               26-JUL-2002
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                                                                                                                                                                                                                                           AAD35726;
   Query Match
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                                                                                                                                                                The present invention describes the rat Nurrl coding and protein sequences. The Nurrl protein is involved in the induction of tyrosine hydroxylase expression in adult rat-derived hippocampal progenitor cells. The Nurrl gene and protein can be used in the treatment of catecholaminerelated diseases such as Parkinson's disease, manic depression and schizophrenia. They can also be used to induce tyrosine hydroxylase expression and identify tyrosine hydroxylase related deficiencies, which are linked to the same diseases. The present sequence is a PCR primer used in a method to differentiate adult neural progenitor cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Antisense; E2F transcription factor 1; human; infection; inflammation;
                                                       Cell comprising exogenous nucleic acid inducing tyrosine hydroxylase expression useful for treating catecholamine-related diseases such as Parkinson's disease, manic depression and schizophrenia.
                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Antisense compound capable of inhibiting the expression of E2F transcription factor 1, useful for preventing or delaying infection,
                                                                                                                                                                                                                                                                                                                                                                                                                              ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human E2F transcription factor 1 antisense oligonucleotide #57
                                                                                                                                                                                                                                                                                                                                                                                        0.4%; Score 16.8; DB 1; Length 20; B5.0%; Pred. No. le+03;
                                                                                                                                                                                                                                                                                                                                                                                                                            1; Indels
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polypeptide comprising a monomer polypeptide with a molecular weight of 30 kDa. p30 is also called LiGHT because this is homologues to cytokine. p30 is also called LiGHT because this is homologues to Lymphotoxine, exhibite Inducible expression, and competes with HSV clycoprotein D for HVEM, a receptor expressed T lymphocytes.p30 binds to lymphotoxin beta receptor expressed T lymphocytes.p30 binds to lymphotoxin beta receptor (LIV SR)-mediated polypeptide (HVEM). p30 is useful for inhibiting virus production in cells and for modulating a lymphotoxin beta receptor (LIV SR)-mediated cellular response. p30 is useful for treating inflammatory disorders, tumours, for blocking the entry of herpes virus info cells, and to treat or prevent chrose virus infections such as beta herpes virus and cytomegalovirus. p30 is also useful for inhibiting p30-mediated cellular response e.g., inhibition of a lymphocyte (a pathogenic effector cell) cellular response cuch as lymphocyte proliferation. The inhibited lymphocyte response modulates a T or B lymphoma or an autoimmune disease such as rheumatoid arthritis, insulin dependent diabetes mellitus, multiple sclerosis,
                   diseases associated with hibeta4BP expression, particularly conditions involving aberrant or deregulated cell proliferation (e.g. cancer). The hibeta4BP polynucleotide is used in gene therapy. The present sequence is an antisense oligonucleotide targetted to hibeta4BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; herpes virus entry-mediated; HVEM; p30; immunosuppressive; tumour; Hufflammatory disorder; herpes virus infection; lymphocyte proliferation; neuroprotective; dermatological; virucide; gene 'therapy; PCR primer; SLE; systemic lupus erythematosus; autoimmune disease; diabetes mellitus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel polypeptide useful for inhibiting herpes virus production in cells, comprises isolated or recombinant homotrimeric p30 polypeptides which bind to lymphotoxin receptor and to herpes virus entry-mediated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            rheumatoid arthritis; multiple sclerosis; myasthenia gravis; LIGHT; ss.
                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to an isolated or recombinant homotrimeric p30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human soluble LIGHT DNA generating mutagenic forward PCR primer #4.
expression. The antisense compounds are useful to prevent or treat
                                                                                                                                                                                                                ö
                                                                                                                                                                    3; DB 1; Length 20; 1e+03;
                                                                                                                                                                                                              2; Indels
                                                                                                                             Sequence 20 BP; 2 A; 4 C; 7 G; 7 T; 0 U; 0 Other;
                                                                                                                                                                                                              0; Mismatches
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                                                                                                                                                                    Score 16.8;
Pred. No. 1e
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                                                                                                                                                                                                                                                        718 AACACCACCGACAAGGAGCT 737
                                                                                                                                                                                                                                                                                AATACCACCGACCAGGAGCT 1
                                                                                                                                                                                                                                                                                                                                                                                                         BP.
                                                                                                                                                                      0.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                         AAD22911 standard; DNA; 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                              18; Conservative
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                                                                                                                                                                    Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                             20
                                                                                                                                                                                                                                                                                                                                                                                                                                                AAD22911;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Identifying a candidate polymorphic repeat within a coding sequence, for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention discloses a method for identifying a candidate polymorphic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     syndrome, Huntington's disease, fragile-X syndrome, Fredreich's ataxis, myotonic dystrophy, hyperandrogenaemia, spinal and bulbar atrophy and spinocerebellar ataxia. The sequences presented in ABX79676-ABX80022 are the polymorphic repeats identified for a search of human ESTs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EST; expressed sequence tag; ss; polymorphic repeat; tandem repeat; polymorphic marker prediction of ubiquitous simple sequences; POMPOUS; Rep-X; human; genetic disease; drug-treatment; Machado-Joseph; Haw River syndrome; Huntington's disease; fragile-X syndrome; Fredreich's ataxis; myotonic dystrophy; hyperandrogenaemia; spinal atrophy; bulbar atrophy; spinocerebellar ataxia.
                                                                                                                                                                               Gaps
                  ase modulates a reaction to a transplant.

App. The present sequence is a mutagenic soluble LIGHT DNA also referred as p30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  understanding or treating genetic disease, comprises detecting trepeats in a target coding sequence and scoring the repeats for
                                                                                                                                                                             ö
  systemic lupus erythematosus (SLE) or myasthenia gravis. Also,
                                                                                                                               Score 16.8; DB 1; Length 20;
Pred. No. 1e+03;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 20 BP; 9 A; 11 C; 0 G; 0 T; 0 U; 0 Other;
                                                                                                BP; 3 A; 6 C; 7 G; 4 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EST polymorphic DNA repeat polynucleotide #337.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fondon JW;
                inhibited lymphocyte response modulates
DNA is useful in gene therapy. The prese
                                                                                                                                                                                                                  2110 AGCTCCAGCTCCTCAGGGGA 2129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example; Col 1165; 588pp; English.
                                                                                                                                                                                                                                                         20 AGCTCCAGCTCCTCGGGGAA 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Minna JD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99US-00475947
                                                                                                                                        0.4%;
                                                                                                                                                        ilarity 90.0%;
Conservative
                                                                                                                                                                                                                                                                                                                                                          ABX80012 standard; cDNA; 20
                                                         primer used for generating
                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       polymorphic probability.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Wren JD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2003-208818/20
                                                                                                                                                        Best Local Similarity
Matches 18; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sapiens.
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                                                                                                Sequence 20
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                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                     RESULT 790
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention relates to novel antisense oligomucleotides (ABZ81522-ABZ81593) which are targeted to human protein kinase A (PKA) regulatory subunit RII beta mucleotide sequence (ABZ81513), and which specifically hybridise with and inhibit the expression of the PKA regulatory subunit RII beta (PKA is also known as cAMP-dependent protein kinase). The antisense oligomucleotides are useful for modulating the kinase). The antisense oligomucleotides are useful for modulating the conditions associated with aberrant expression of PKA regulatory subunit RII beta, e.g. diabetes or cancer. The antisense compounds are also useful for diagnostics, therapeutics, prophylaxis, e.g. to prevent or delay infection, inflammation or tumour formation, as research reagents and kits, and in distinguishing between functions of various members of a biological pathway
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New antieense oligonucleotides targeted to nucleic acid encoding protein
kinase A regulatory subunit RII beta, useful in treating diseases e.g.
cancer associated with the aberrant expression of the protein kinase.
                                                                                                                                                                                                                                                                                                 PKA regulatory subunit RII beta antisense oligonucleotide ISIS #114458
                                                                                                                                                                                                                                                                                                                                 Human, cytostatic, antidiabetic, antisense therapy, phosphorothioate, protein kinase inhibitor; protein kinase A, PKA; regulatory subunit RII beta; cAMP-dependent protein kinase; diabetes; cancer; infection; inflammation; tumour; ss.
                                    Gaps
                                    ö
 Length 20;
Score 16.8; DB 1; Length 2 Pred. No. 1e+03; 0; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                        TGGTCTGTGTGTGTGTGT 2332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /mod_base= OTHER
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                                                                                                       20 receptorererererer
                                                                                                                                                                                              BP.
     0.4%;
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                                                                                                                                                                                              ABZ81533 standard; DNA; 20
                                                                                                                                                                                                                                                                  26-AUG-2003 (first entry)
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     Query Match
Best Local Similarity 90.0
Matches 18; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             modified base
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                                                                                                                                                                                                                                                                                                                                                                                                                            Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Monia BP,
                                                                          2313
                                                                                                                                                                                                                                   ABZ81533;
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The invention relates to a novel pharmaceutical composition, which has a first active agent comprising an oligonucleotide antisense to the initiation codon, coding region, 5' or 3' end genomic flanking regions, 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of junctions of genes encoding a polypeptide associated with lung and/or nasal airway dysfunction and a second active agent comprising an entitlanmatory steroid and ubiquinone. A composition of the invention has antiinflammatory antiallergic, antiasthmatic, hypotensive, commonsuppressive, and cytostatic activity. The composition may have a immunosuppressive, and cytostatic activity. The composition may have a use in antisense gene therapy. The composition is useful for treating or correction a respiratory lung or malignant disease or condition, also for enhancing the prophylactic or therapeutic respiratory effect of an antiallammatory steroid in a subject, for reducing levels of adenosine or receptor, producing bronchodilation, increasing levels of adenosine creceptor, producing bronchodilation, increasing levels of ubiquinone or lung inflammation, lung allergies, or a respiratory disease or condition. Once: The sequence data for this patent is not represented in the printed specification, but was obtained in electronic format directly from WIPO at the control of the control 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pharmaceutical composition for treating ailments associated with impaired
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; antisense; lung dysfunction, nasal airway dysfunction; antilnflammatory steroid; ubiquinone; antilnflammatory; antiallergic; antiatethmatic; hypotensive; immunosuppressive; cytostatic; gene therapy; antisense gene therapy; respiratory; lung; adenosine sensitivity; adenosine receptor; bronchodilation; bronchoconstriction; lung allergy; lung inflammation; respiratory disease; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           respiration, has oligo(s) antisense to specific gene(s) or its corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid
                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pabalan J, Aguilar D;
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                               Indels
                               2;
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       90.0%; Pred. No. 1e+03;
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                               0; Mismatches
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, Shahabuddin S;
                                                                                177 CGAAGACGGGGAGGACGAGG 196
                                                                                                                                                                                                                                                                                                                                                                                                          Human oligonucleotide sequence.
                                                                                                                                 20 cchgchccccchachcchcchcc
                                                                                                                                                                                                                                                           ВР.
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                                                                                                                                                                                                                                                         ABZ89549 standard; DNA; 20
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                                 18; Conservative
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Tang L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2003-229219/22.
Best Local Similarity
Matches 18; Conserv
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Miller S,
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                                                                                                                                                                                                                                                                                                            ABZ89549;
                                                                                                                                                                                                            RESULT 792
                                                                                                                                                                                                                                      ABZ89549
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Query Match

DB 1; Length 20;

0.4%; Score 16.8;

Query Match

vivlemore401-10.rng

ö Gaps ö 2; Indels Pred. No. 1e+03; 0; Mismatches Best Local Similarity 90.0%; Matches 18; Conservative

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RESULT 793 AB284884

ABZ84884 standard; DNA; 20 BP

ABZ84884;

(first entry) 17-OCT-2003 Human oligonucleotide sequence.

Human; antisense; lung dysfunction; nasal airway dysfunction; antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic; antiasthmatic; hypotensive; immunosuppressive; cycostatic; gene therapy; antisense gene therapy; respiratory; lung; adenosine sensitivity; adenosine receptor; bronchodilation; bronchoconstriction; lung allergy; lung inflammation; respiratory disease; ds.

Homo sapiens

WO200285308-A2

31-OCT-2002

23-APR-2002; 2002WO-US013135.

24-APR-2001; 2001US-0286137P

(EPIG-) EPIGENESIS PHARM INC

Aguilar Katz E, Pabalan J, Li Y, Sandrasagra A, Ka Tang L, Shahabuddin S; Miller S, Nyce JW,

WPI; 2003-229219/22

Pharmaceutical composition for treating ailments associated with impaired respiration, has oligo(s) antisense to specific gene(s) or its corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or ubiquinone

Claim 15; SEQ ID NO 126; 872pp; English.

The invention relates to a novel pharmaceutical composition, which has a first active agent comprising an oligonucleotide antisense to the initiation codon, coding region, 5 or 3 end genomic flanking regions, 5 and 3' intron-exon junctions, or regions within 2-10 nucleotides of junctions of genes encoding a polypeptide associated with lung and/or nasal airway dysfunction and a second active agent comprising an antiinflammatory steroid and ubiquinone. A composition of the invention has antiinflammatory and cytostatic activity. The composition may have a use in antisense gene therapy. The composition is useful for treating or preventing a respiratory, lung or malignant disease or condition, also for enhancing the prophylactic or therapeutic respiratory effect of an antiinflammatory steroid in a subject, for reducing or depleting levels of, or reducing sensitivity to adenosine, reducing levels of, or reducing sensitivity to adenosine, reducing levels of useful or receptor, producing bronchodilation, increasing levels of usigninone or lung surfactant in a subject's tissue, or treating bronchoconstriction, lung inflammation, lung allergies, or a respiratory disease or condition. Note: The sequence data for this patent is not represented in the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences

Sequence 20 BP; 0 A; 7 C; 4 G; 9 T; 0 U; 0 Other;

Query Match

DB 1; Length 20; 0.4%; Score 16.8;

ö Gaps ö Indels ; 7 Pred. No. 1e+03; 0; Mismatches 3644 GCTGTCCCTTGCTTGCTGC 3663 1 GCTGTCCCTTTTTGCCTGC 20 90.08; Local Similarity 90.0 nes 18; Conservative Best Loca Matches ð 셤

RESULT 794 ABZ8807

BP. ABZ88076 standard; DNA; 20

ABZ88076;

(first entry) 17-0CT-2003

Human oligonucleotide sequence

Human; antisense; lung dysfunction; nasal airway dysfunction; antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic; antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy; antisense gene therapy; respiratory; lung; adenosine sensitivity; adenosine receptor; bronchodilation; bronchoconstriction; lung allergy; lung inflammation; respiratory disease; ds.

Homo sapiens.

WO200285308-A2

23-APR-2002; 2002WO-US013135.

24-APR-2001; 2001US-0286137P

(EPIG-) EPIGENESIS PHARM INC

Aguilar D; Pabalan J, Katz B, Shahabuddin S; Sandrasagra A, Tang L, Li Y, Nyce JW, 1

WPI; 2003-229219/22

Pharmaceutical composition for treating ailments associated with impaired respiration, has oligo(s) antisense to specific gene(s) or its corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or ubiquinone

Disclosure; SEQ ID NO 3318; 872pp; English.

The invention relates to a novel pharmaceutical composition, which has a first active agent comprising an oligonucleotide antisense to the initiation coodon, coning region, 5 or 3' end genomic flanking regions, 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of junctions of genes encoding a polypeptide associated with lung and/or nasal airway dysfunction and a second active agent comprising an antiinflammatory steroid and ubiquinone. A composition of the invention has antiinflammatory, antiallergic, antiasthmatic, hypotensive, immunosuppressive, and cytostatic activity. The composition may have a use in antisense gene therapy. The composition is useful for treating or preventing a respiratory, lung or malignant disease or condition, also for enhancing the prophylactic or therapeutic respiratory effect of an antiinflammatory steroid in a subject, for reducing levels of adenosine of receptor, producing bronchodilation, increasing levels of adenosine or receptor, producing bronchodilation, increasing levels of defence of the receptor. lung surfactant in a subject's tissue, or treating bronchoconstriction, lung inflammation, lung allergies, or a respiratory disease or condition. Note: The sequence data for this patent is not represented in the printed specification, but was obtained in electronic format directly from WIPO ftp.wipo.int/pub/published_pct_sequences

Sequence 20 BP; 6 A; 5 C; 6 G; 3 T; 0 U; 0 Other;

Query Match

DB 1; Length 20; 0.4%; Score 16.8;

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Gaps

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Pharmaceutical composition for treating ailments associated with impaired respiration, has oligo(s) antisense to specific gene(s) or its corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to a novel pharmaceutical composition, which has a first active agent comprising an oligonucleotide antieense to the initiation codon, coding region, 5 or 3 end genemic flanking regions, 5 and 3' intron-exon junctions, or regions within 2-10 nucleotides of junctions of genes encoding a polypeptide associated with lung and/or nasal airway dysfunction and a second active agent comprising an antinflammatory steroid and ubiquinone. A composition of the invention has antiinflammatory, antiallergic, antiasthmatic, hypotensive, immunosuppressive, and cytostatic activity. The composition may have a use in antisense gene therapy. The composition is useful for treating or preventing a respiratory, lung or malignant disease or condition, also for enhancing the prophylactic or therapeutic respiratory effect of an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human, antisense; lung dysfunction; nasal airway dysfunction; antinflammatory steroid; ubiquinone; antinflammatory; antiallergic; antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy; antisense gene therapy; respiratory; lung; adenosine sensitivity; adenosine receptor; bronchodilation; bronchoconstriction; lung allergy; lung inflammation; respiratory disease; ds.
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Pred. No. 1e+03;
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                                   0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human PDE4A oligonucleotide sequence.
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                                                                                              1876 GAGGAGCTCTTCAAGCTGCT 1895
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   90.08;
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                                   18; Conservative
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Tang L,
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   Best Local Similarity
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ABZ98946/c
                                   Matches
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DB 1; Length 20;

0.4%; Score 16.8;

Query Match

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel isolated nucleic acid fragment encoding a tuliposide A synthesizing protein, useful for creating recombinant organisms that have the ability to synthesize tulipalin A, tuliposide A or tuliposide A pathway intermediates.
                                                                                                                                                                                                                                                                                                                    Alpha-methylene-gamma-butyrolactone; glutamate decarboxylase; herbicide; enzyme; gamma-aminobutyrate aminotransferase; UDP-glucosyltransferase; gamma-hydroxybutyrate dehydrogenase; tulipalin A; plant; primer; PCR; ss.
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                  Gaps
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                    Indels
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                  2;
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   90.0%; Pred. No. 1e+03;
iive 0; Mismatches
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                                                       1886 TCAAGCTGCTGAAGGAGGC 1905
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ABD24306
ID ABD24306 standard; DNA; 20
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                    18; Conservative
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Best Local Similarity
Matches 18; Conserv
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ABD24306;

(first entry) 29-JUL-2004 AI095013-derived oligonucleotide DNA SEQ ID 3318.

Human; antisense; bronchoconstriction; allergy; hyposecretion; pain; respiratory tract inflammation; adenosine sensitivity; lung; cancer; surfactant depletion; antiallergic; antiinflammatory; antiasthmatic; analgesic; hypotensive; immunosuppressive; cytostatic; cystic fibrosis; beta-adrenergic agonist; respiratory disease; pulmonary vasoconstriction; respiratory distress syndrome; allergic fibritis; pulmonary bypertension; emphysema; chronic obstructive pulmonary disease; cancer; bronchitis; pulmonary transplantation rejection; ss; primer.

Homo sapiens

WO200285309-A2

31-OCT-2002

23-APR-2002; 2002WO-US013143.

24-APR-2001; 2001US-0286036P.

(EPIG-) EPIGENESIS PHARM INC

Katz E, Pabalan J, Aguilar D; Li Y, Sandrasagra A, Ka Tang L, Shahabuddin S; Miller S, Nyce JW,

WPI; 2003-093058/08.

to Pharmaceutical composition for treating asthma, has antisense oligonuclectide containing less percentage of adenosine, targeted tnucleic acids associated with lung airway or lung dysfunction, and bronchodilating agent.

Claim 15; SEQ ID NO 3318; 763pp; English.

This invention describes a novel composition (a) a first active agent, comprising oligonucleotides, effective for alleviating bronchoconstruction, respiratory tract inflammation, allergies and bronchoconstruction, respiratory tract inflammation, allergies and condition depolation or hyposecretion, when administered to a mammal. The oligonucleotides are derived from a gene encoding or regulating expression of a target polypeptide associated with lung airway or lung dysfunction or cancer and can be anti-sense to the corresponding mRNA. The invention also describes a kit, that comprises: (a) a delivery device, in separate containers, (b) the oligonucleotides, (c) instructions for adding a carrier and for use of the kit. The composition of the invention has antiallergic, antinflammatory, antiasthmatic, analgesic, hypotensive, immunosuppressive and cytostatic activity, is a beta-drenergic agonist. The composition is useful for preventing or treating a respiratory, lung or malignant disease. The administered composition comprises oligo and is administered to reduce the production or reduce the amount of target polypeptide present in the lungs. The pulmonary obstruction, and/or bronchoconstriction and/or lung inflammation, allergies, asthma, impeded respiration, respiratory distress syndrome, pain, cystic fibrosis, allergic rhinitis, pulmonary hypertension, emphysema, chronic obstructive pulmonary disease, pulmonary transplantation rejection, pulmonary infections, bronchitis or cancer. The reduced adenosine content of the anti-sense oligos corresponding to thymidines present in the target RNA serves to prevent the breakdown of the oligonucleotides into products that free adenosine into the system e.g., lung, brain, heart, kidney, etc, tissue environment and thereby, to inflammation, allergies and/or surfactant hypoproduction are associated with a disease or condition such as pulmonary vasoconstriction, prevent any unwanted effects due to it

Sequence 20 BP; 6 A; 5 C; 6 G; 3 T; 0 U; 0 Other;

ô comprising oligonucleotides, effective for alleviating bronchocometriction, respiratory tract inflammation, allergies and reducing adenosine sensitivity, levels of adenosine (A) or (A) receptors, surfactant depoletion or hyposecretion, when administered to a mammal. The oligonucleotides are derived from a gene encoding or regulating expression of a target polypeptide associated with lung airway or lung dysfunction or cancer and can be anti-sense to the corresponding mkNA. The invention also describes a kit, that comprises: (a) a delivery device, in separate containers, (b) the oligonucleotides, (c) instructions for adding a carrier and for use of the kit. The composition of the invention has antiallergic, antiinflammatory, antiasthmatic, beta addrensive, immunosuppressive and cytostatic activity, is a beta-addrenergic agonist. The composition is useful for preventing or treating a respiratory, lung or malignant disease. The administered respiratory tract inflammation; adenosine sensitivity; lung; cancer; surfactant depletion; antiallergic; antiinflammatory; antiasthmatic; antiandsessive; cytostatic; cyetic fibrosis; beta-adrenergic agonist; respiratory disease; pulmonary vasoconstriction; respiratory disease; pulmonary vasoconstriction; emphysema; chronic obstructive pulmonary disease; cancer; bronchitis; pulmonary transplantation rejection; ss; primer. composition comprises oligo and is administered to reduce the production or availability, or to increase the degradation of the target mRNA or to reduce the amount of target polypeptide present in the lungs. The pulmonary obstruction, and/or bronchoconstriction and/or lung inflammation, allergies and/or surfactant hypoproduction are associated with a disease or condition such as pulmonary vasoconstriction, This invention describes a novel composition (a) a first active agent Gaps S antisense, bronchoconstriction, allergy, hyposecretion, pain, Pharmaceutical composition for treating asthma, has antisense oligonucleotide containing less percentage of adenosine, targeted trucleic acids associated with lung airway or lung dysfunction, and Katz E, Pabalan J, Aguilar D; ö Length 20; Indels Score 16.8; DB 1; Pred. No. 1e+03; 0; Mismatches 2; Human PDE4A-derived oligonucleotide SEQ ID 14188. Claim 15; SEQ ID NO 14188; 763pp; English. ŝ 1876 GAGGAGCTCTTCAAGCTGCT 1895 1 GAGGAGCTCAACAAGCTGCT 20 Li Y, Sandrasagra A, Tang L, Shahabuddin BP 0.4%; 23-APR-2002; 2002WO-US013143. 24-APR-2001; 2001US-0286036P. (EPIG-) EPIGENESIS PHARM INC. ABD31977 standard; DNA; 20 (first entry) Query Match
Best Local Similarity 90.0
Matches 18; Conservative oronchodilating agent WPI; 2003-093058/08. WO200285309-A2. Homo sapiens. 29-JUL-2004 31-OCT-2002. Nyce JW, 1 Miller S, ABD31977; RESULT 798 g

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inflammation, allergies, asthma, impeded respiration, respiratory distress syndrome, pain, cystic fibrosis, allergic rhinitis, pulmonary hypertension, emphysema, chronic obstructive pulmonary bleases, pulmonary transplantation rejection, pulmonary infections, bronchitis or cancer. The reduced adenosine content of the anti-sense oligos corresponding to thymidines present in the target RNA serves to prevent the breakdown of the oligonuclectides into products that free adenosine into the system e.g., lung, brain, heart, kidney, etc, tissue environment and thereby, to prevent any unwanted effects due to it
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This invention describes a novel composition (a) a first active agent, comprising oligonuclectides, effective for alleviating bronchoconstriction, respiratory tract inflammation, allergies and reducing adenosine sensitivity, levels of adenosine (A) or (A) receptors, surfactant depletion or hyposecretion, when administered to a mammal. The oligonuclectides are derived from a gene encoding or regulating expression of a target polypeptide associated with lung airway or lung dysfunction or cancer and can be anti-sense to the corresponding mRNA. The invention also describes a kit, that comprises: (a) a delivery
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         analgesic; hypotensive; immunosupressive; cytostatic; cystic fibrosis; beta-adrenergic agonist; respiratory disease; pulmonary vasoconstriction; respiratory distresses syndrome; allergic rhinitis; pulmonary hypertension; emphysema; chronic obstructive pulmonary disease; cancer; bronchitis; pulmonary transplantation rejection; ss; primer.
                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human, antisense, bronchoconstriction, allergy, hyposecretion, pain, respiratory tract inflammation, adenosine sensitivity, lung, cancer, surfactant depletion, antiallergic, antiinflammatory, antiasthmatic,
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                                                                                                                                                                                                              Sequence 20 BP; 3 A; 7 C; 5 G; 5 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 15; SEQ ID NO 126; 763pp; English
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L, Shahabuddin
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, Tang L,
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instructions for adding a carrier and for use of the kit. The composition of the invention has antiallergic, antinflammatory, antiasthmatic, analgesic, hypotensive, immunosuppressive and cytostatic activity, is a beta-adrenergic agonist. The composition is useful for preventing or treating a respiratory, lung or malignant disease. The administered composition comprises oligo and is administered to reduce the production or availability, or to increase the degradation of the target mRNA or to reduce the amount of target polypeptide present in the lungs. The pulmonary obstruction, and/or bronchocomstriction and/or lung inflammation, allergies and/or surfactant hypoproduction are associated with a disease or condition such as pulmonary vasoconstriction, inflammation, allergies, asthma, impeded respiration, respiratory distructs pain, cystic fibrosis, allergic rhintis, pulmonary transplantation rejection, pulmonary infections, bronchitis or cancer. The reduced adenosine content of the anti-sense oligos corresponding to the pulmonary intention rejection, pulmonary infections, bronchitis or cancer. The reduced adenosine content of the anti-sense oligos corresponding to the pulmonary intention speam into products that free adenosine into the system of the vilgonucleotides into products that free adenosine into the system of prevent any unwanted effects due to it
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; antisense; bronchoconstriction; allergy; hyposecretion; pain; respiratory tract inflammation; adenosine sensitivity; lung; cancer; surfactant depletion; antiallergic; antiinflammatory; antiasthmatic; analgesic; hypotensive; immunosuppressive; cytostatic; cystic fibrosis; beta-adrenargic agonist; respiratory disease; pulmonary vasoconstriction; respiratory distress syndrome; allergic rhinitis; pulmonary hypertension; emphysema; chronic obstructive pulmonary disease; cancer; bronchitis;
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nucleic acids associated with lung airway or lung dysfunction, and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0.4%; Score 16.8; DB 1; Length 20; 90.0%; Pred. No. 1e+03; tive 0; Mismatches 2; Indels
in separate containers, (b) the oligonucleotides,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pabalan J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Seguence 20 BP; 0 A; 7 C; 4 G; 9 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         pulmonary transplantation rejection; ss; primer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AI085559-derived oligonucleotide SEQ ID 4791.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3644 GCTGTCCCTTGCTTGCTGC 3663
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24-APR-2001; 2001US-0286036P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABD25779 standard; DNA; 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29-JUL-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2003-093058/08.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Li Y, San
Tang L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
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Miller S,
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94US-00309335. 95US-00531241. 99US-00263959

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including autoimmune diseases, degenerative nervous system diseases, cardiversus host diseases, hypersensitivity diseases, infectious diseases, and neeplastic diseases. Autoimmune diseases, infectious diseases and neeplastic diseases. Autoimmune diseases, include Addison's diseases, arrophic gastritis. Degenerative nervous system diseases include multiple sclerosis and Alzheimer's disease. Hypersensitivity diseases include Type is hypersensitivities such as those present in Goodpasture's syndrome and Type IV hypersensitivities such as those caused by viruses such as Hypersensitivities such as those caused by viruses such as Hose caused by viruses such as Hose caused by viruses such as those caused by viruses such as those caused by the yeast genus Candida, parasitic infections such as those caused by Mycobacterium. Neoplastic diseases include lymphoproliferative diseases such as leukaemias, lymphomas and cancers such as cancer of the brain, breast. The present sequence represents a Vbeta gene repeat sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        autoimmune, degenerative nervous system and infectious disease, comprises nucleic acid primers specifically priming and allowing amplification of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to a kit for diagnosing and treating T-cell associated diseases which comprises a panel of nucleic acid primers specifically priming and allowing amplification of each Vbeta gene, VbetaRNA or CDNA. The kit is useful for diagnosing organ transplant rejection and diagnosing and treating T-cell associated diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kit for diagnozing and treating T-cell associated diseases e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 20 BP; 8 A; 0 C; 0 G; 12 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; SEQ ID NO 596; 164pp; English.
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Best Local Similarity 90.0
Matches 18; Conservative
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                                                                                                                                                                                                                           HOOD/) HOOD L E.
                                                                                                                                                                                                                                                                    (ROWE/) ROWEN L.
                                05-MAR-1999;
                                                                                                             19-SEP-1994;
                                                                                                                                                      19-SEP-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Vbeta gene
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                                                                                                                              This invention describes a novel composition, alleriating active agent, comprising oligonuclectides, effective for alleviating bronchoconstriction, respiratory tract inflammation, allergies and bronchoconstriction, respiratory tract inflammation, allergies and concedence sensitivity, levels of adenosine (A) or (A) receptors, surfactant depletion or hyposecretion, when administered to a mammal. The oligonuclectides are derived from a gene encoding or regulating expression of a target polypeptide associated with lung airway or lung dysfunction accorder and can be anti-sense to the corresponding mRNA.

The invention also describes a kit, that comprises: (a) a delivery device, in separate containers, (b) the oligonuclectides, (c) instructions for adding a carrier and for use of the kit. The composition of the invention has antiallargic, antiinflammacory, antiasthmatic, analgesic, hypotensive, immunosuppressive and cytostatic activity, is a beta-adrenergic agonist. The composition is useful for preventing or treating a respiratory, lung or malignant disease. The administered composition comprises oligo and is administered to reduce the production or the lungs. The pulmonary obstruction, and/or bronchoconstriction and/or lung corresponding to inflammation, allergies and/or surfactant hypoproduction are associated with a disease or condition such as pulmonary vasoconstriction, confined and submanation, allergies, asthma, impeded respiration, respiratory distress syndrome, pain, cystic fibrosis, allergic rhinitis, pulmonary transplantation rejection, pulmonary infections, bronchitis or cancer. The reduced adenosine content of the anti-sense oligos corresponding to the oligonucleotides into products that free adenosine into the system correction and unique to it the oligonucleotides into products that free adenosine into the system correct of the oligonucleotides into product expect to it.
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                                                                                                             This invention describes a novel composition (a) a first active agent,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1e+03;
hes 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 20 BP; 1 A; 2 C; 8 G; 9 T; 0 U; 0 Other;
                                    Claim 15; SEQ ID NO 4791; 763pp; English.
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ADH70402
ID ADH70402
XX
AC ADH704
XX
DT 25-MAR
DE Human;
XX
Human
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                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                        human; T-cell associated disease; Vbeta; autoimmune disease;
0.4%; Score 16.8; DB 1; Length 20; 90.0%; Pred. No. 1e+03; tive 0; Mismatches 2; Indels
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                                                                                                                                                                                                      RESULT 802
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Addison's disease, atrophic gastritis, degenerative nervous system disease; multiple sclerosis, degenerative nervous system disease; multiple sclerosis, allzenses, type I hypersensitivity doodpasture's syndrome; type II hypersensitivity; doodpasture's syndrome; type IV hypersensitivity; leprosy; infectious disease; viral infection; HIV; fungal infection, Candida; parasitic infection; schistosome; filaria; bacterial infection; Mycobacterium; neoplastic disease; lymphoproliferative disease; leukaemia; lymphoma; cancer; brain cancer;

breast cancer; ds

US2002150891-A1 ното варіепв

17-OCT-2002

human; T-cell associated disease; Vbeta; autoimmune disease; degenerative nervous system disease; graft versus host disease; hypersensitivity disease; infectious disease; neoplastic disease;

Human Vbeta gene repeat sequence #192.

25-MAR-2004 (first entry)

ADH70402;

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This invention describes novel oligonuclectides derived from microsatellite markers and used for the amplification of the rose genome. The invention also describes a test kit for genetic analysis of cultured cor wild forms of the genus Rosa sp. that contains at least one of the new coligonuclectide primers and preparing microsatellite markers of Rosa sp. by PCR amplification of hypervariable genomic regions, using at least one primer pair, to produce polymorphic fragments which are separated and detected. The primer pairs flank the microsatellite locus being amplified. The amplified markers are separated by electrophoresis, cespecially on high-resolution agarose or native or denatured polyacrylamide gels, or by mass spectrometry. After separation, the amplicons are detected by staining (ethidium bromide or silver), radioactive labelling and autoradiography, automated sequencing using primers labelled with dyes or fluorophores or by mass spectrometry. A cadioactive labelling and autoradiography, automated sequencing using primers labelled with dyes or fluorophores or by mass spectrometry. A cadioactive detected by staining (ethidium bromide or silver), coli and the cells tested against a high-density array of synthetic microsatellites. Inserts in plasmids that hybridised were sequenced and microsatellites. Inserts in plasmids that hybridised were sequenced and the introvated and wild types of roses, particularly for genetic mapping and labelling of mono- or poly-genic traits, selection, analysis of cultivated and wild types of roses, particularly for genetic or radioactive detection methods and can differentiate between a compined or methods and can differentiate between almost all commercial rose varieties. ADH68375 ADH68474 represent the PCR primers commercial rose varieties. ADH68474 represent the PCR primers contents.
                                                                                                                                                                                                                                                                                                                                                                                                                                    New oligonucleotides from rose microsatellite markers, useful for genomic analysis, including identification of varieties and hybrids.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; Page 11; 52pp; German.
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                                                                                                                                                                                                                     17-MAY-2002; 2002DE-01022632.
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11 Similarity 90.0%;
18; Conservative (
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                                                      WO2003097869-A2.
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                                                                                                          27-NOV-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADJ60829,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to a kit for diagnosing and treating T-cell associated diseases which comprises a panel of mucleic acid primers specifically priming and allowing amplification of each Wbeta gene, whetars. The kit is useful for diagnosing organ transplant crejection and diagnosing and treating T-cell associated diseases including autoimmune diseases, degenerative nervous system diseases, cor graft versus host disease, Autoimmune diseases include Addison's diseases. Cor artophic gastritis. Degenerative nervous system diseases include multiple artophic gastritis. Degenerative nervous system diseases include multiple cor sclerosis and Alzhehmer's disease. Hypersensitivity diseases include multiple is sclerosis and Alzhehmer's disease. Hypersensitivities such as those conformed in leprosy. Infections such as those present in Goodpasture's syndrome and Type IV hypersensitivities such as those caused by the yeast genus Candida, parasitic infections such as those caused by the yeast genus Candida, parasitic infections such as those caused by Mycobacterium. Neoplastic diseases include viral infections such as those caused by Mycobacterium. Neoplastic diseases include a such as those caused by whochacterium. Neoplastic diseases include lymphoproliferative diseases couch as leukaemias, lymphomas and cancers such as cancer of the brain, becaut. The present sequence represents a Vbeta gene repeat sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kit for diagnozing and treating T-cell associated diseases e.g. autoimmune, degenerative nervous system and infectious disease, comprises nucleic acid primers specifically priming and allowing amplification of a Vbeta gene.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 20 BP; 8 A; 0 C; 0 G; 12 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; SEQ ID NO 596; 164pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2004-059052/06.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hood LE, Rowen L;
     breast cancer; ds.
                                                                                                                                                                                                                                                                                                                                                                  (HOOD/) HOOD L E.
                                                                                                                                                                                                                                                                                                                                                                                               (ROWE/) ROWEN L.
                                                                                                                US2002150891-A1
                                                                                                                                                                                                                             05-MAR-1999;
                                                                                                                                                                                                                                                                                 19-SEP-1994;
                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                           19-SEP-1995;
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                                                                                                                                                                       17-OCT-2002.
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Query Match

Matches

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ADH68620;

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Score 16.8; DB 1; Length 20;
Pred. No. 1e+03;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                interleukin; IL-4 receptor; IL-5 receptor; lung disease;
                                                                                                                                                                                                                                                                                                                                                                      Oligonucleotide associated to PDE4A #112.
                                                                                             2337 GIGIGIGIGIGIGACAT 2356
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                                                                                                                                                                                                                                                                                                                                                                                             The present invention relates to an oligonucleotide anti-sense to e.g., initiation codon, coding region with 2-10 nucleotides of 5'-end and 3'-end of nucleic acid target comprising gene(s) chosen from e.g. interleukin (IL)-4 receptor, IL-5 receptor or salts of the oligonucleotide and optionally surfactant operatively linked to the oligonucleotide. The method is useful for preventing or treating a respiratory or lung disease, which involves administering to the airways of a subject an effective amount of an inhibitor. The oligonucleotide is useful for production of a medicament for the prevention and/or treatment of a respiratory or lung disease. The respiratory or lung disease is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    chosen from airway inflammation, allergy(ies), asthma, impeded respiration, cystic fibrosis (CF), chronic obstructive pulmonary diseases (COPD), allergic rhintis (AR), acute respiratory distress syndrome (ARDS), pulmonary hypertension, lung inflammation, bronchitis, airway obstruction. The present sequence represents an oligonucleotide of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       chimeric; antisense oligonucleotide; phosphorothioate; human; microsomal prostaglandin E2 synthase; mPGES-1; mPGES-1 inhibitor; microsomal prostaglandin E2 synthase inhibitor; cytostatic; antidiabetic; immunomodulator; cardiant; neuroprotective; antiinflammatory; neuroprotective; nootropic; antiathitic; vasotropic; ophthalmological; immunomodulatory; cardiovascular; gene therapy; inflammation;
                                                                                                                                                                                                                                                                                                   Novel single or multiple target oligonucleotide anti-sense to e.g. initiation codons and introns of respiratory disease-relevant genes e.g., CCRI, RANTES, MCP4, useful for prophylaxis or treating respiratory
           cystic fibrosis; acute respiratory distress syndrome; pulmonary hypertension; lung inflammation; bronchitis; oligonucleotide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human mPGES-1 chimeric antisense oligonucleotide SEQ ID NO:1388.
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Pred. No. 1e+03;
0; Mismatches 2; Indels
airway inflammation; allergy; asthma; impeded respiration;
                                                                                                                                                                                                                                Aguilar D, Miller S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 20 BP; 3 A; 7 C; 5 G; 5 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                     Claim 2; SEQ ID NO 1685; 85pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1886 TCAAGCTGCTGAAGGAGGGC 1905
                                                                                                                                                                                                                                Nyce JW, Tang L, Sandrasagra A,
Shahabuddin S, Lu H, Cong H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20 rchaecrecrecadeade 1
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                                                                                                                                                                                                     (EPIG-) EPIGENESIS PHARM INC.
                                                                                                                                                 25-JUL-2003; 2003WO-US023509
                                                                                                                                                                            29-JUL-2002; 2002US-0399076P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           90.06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-JUL-2004 (first entry)
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Best Local Similarity 90.0
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                            disease e.g., asthma.
                                                                                                                                                                                                                                                                          WPI; 2004-203534/19.
                                                                                           WO2004011613-A2.
                                                                  Homo sapiens.
                                                                                                                      05-FEB-2004.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           invention.
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ADM15201/c
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The present sequence represents a chimeric antisense oligonucleotide targeted to human microscomal prostaglandin E2 synthase (mEGES-1). The human megES-1 gene is located on chromosome 9, more specifically to ogg4.3. The present invention also describes: (1) antisense compounds, having a sequence comprising 8-30 bp targeted to a nucleic acid encoding meGES-1, which specifically pybridise with the nucleic acid encoding inhibits its expression; (2) a method of inhibiting the expression of mPGES-1 in cells or tissues; and (3) a method of treating an animal white a disease or condition associated with mPGES-1. MPGES-1 chimeric antidabetic, immunomodulator, cardiant, neuroprotective, antidiabetic, immunomodulator, cardiant, neuroprotective, ophthalmological, immunomodulatory and cardiovascular activities, and can be used as mPGES-1 inhibitors and in gene therapy. The antisense compound can be used as mPGES-1 inhibitors and in gene therapy. The antisense compound con the used as mPGES-1 inhibitors and in gene therapy. The antisense compound con the used as mPGES-1 inhibitors and in gene therapy. The antisense compound condition associated with mPGES-1 e.g., inflammation, Alzheimer's diabetes, cancer, isochaemia or reperfusion injury, or ophthalmic, immunological, cardiovascular or neurological disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New antisense compound, having a sequence targeted to a nucleic acid encoding mPGES-1, useful for preparing a composition for treating e.g., inflammation, Alzheimer's disease, arthritis, diabetes, cancer or
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                                                                                                                                                                                                                                                                                                                                                          /mod_base= OTHER
/note= "phosphorothioate linkages and all cytidine.
residues are 5-methylcytidines"
Alzheimer's disease, arthritis, diabetes, cancer, ischaemia, reperfusion injury, ophthalmic disorder, immunological disorder, cardiovascular disorder, neurological disorder, ss.
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/note= "2'-O-methoxyethyls"
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/note= "2'-O-methocyethyls"
16. .20
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                                                                                                                                                                                                                                                        Location/Qualifiers
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/*tag=
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                                                                                                                                                   Homo sapiens.
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                                                                                                                                                                                 Synthetic.
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                                                                                                                          chimeric; antisense oligonucleotide; phosphorothioate; human; microsomal prostaglandin E2 synthase; mPGES-1; mPGES-1 inhibitor; microsomal prostaglandin E2 synthase inhibitor; cytostatic; antidiabetic; immunomodulator; cardiant; neuroprotective; antiinflammatory; neuroprotective; antiinflammatory; neuroprotective; antiinflammatory; neuroprotective; assotropic; ophthalmological; immunomodulatory; cardiovascular; gene therapy; inflammation; Alzheimer; disease; arthritis; diabetes; cancer; ischaemia; reperfusion injury; ophthalmic disorder; immunological disorder; cardiovascular disorder; neurological disorder; se.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New antisense compound, having a sequence targeted to a nucleic acid encoding mPGES-1, useful for preparing a composition for treating e.ginflammation, Alzheimer's disease, arthritis, diabetes, cancer or
                                                                                                                                                                                                                                                                                                                                               /note= "phosphorothioate linkages and all cytidine residues are 5-methylcytidines"
                                                                                                    Human mPGES-1 chimeric antisense oligonucleotide SEQ ID NO:1396.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     /mod_base= OTHER
/note= "2'-0-methoxyethyls"
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/note== "2'-O-methocyethyls"
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                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                     base= OTHER
                          ADM15209 standard; DNA; 20 BP.
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                                                                            01-JUL-2004
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                                                                                                                                                                                                                                                                        Synthetic.
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                                                    ADM15209;
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 RESULT 806
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              ADM15209,
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can be used for preparing a composition for treating a disease or condition associated with mPGES-1 e.g., inflammation, Alzheimer's disease, arthritis, diabetes, cancer, ischaemia or reperfusion injury,
                                                                                                                                                                                                                                                  Gaps
                                                                             ophthalmic, immunological, cardiovascular or neurological disorder
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "phosphorothioate linkages and all cytidine residues are 5-methylcytidines"
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0
                                                                                                                                                                                    0.4%; Score 16.8; DB 1; Length 20; 90.0%; Pred. No. 1e+03; ive 0; Mismatches 2; Indels
                                                                                                                                     BP; 8 A; 9 C; 3 G; 0 T; 0 U; 0 Other,
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/note= "2'-O-methoxyethyls"
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                                                                                                                                                                                                                                               18; Conservative
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                                                                                                                                                                                             Query Match
Best Local Similarity
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modified_base
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                                                                                                                                        Sequence 20
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                                                                                                                                                                                                                         Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                      807
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADM14960/c
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                        The present sequence represents a chimeric antisense oligonucleotide targeted to human microsomal prostaglandin E2 synthase (mPGES-1). The human mPGES-1 gene is located on chromosome 9, more specifically to ogd4.3. The present invention also describes: (1) antisense compounds, having a sequence comprising 0.30 by targeted to a nucleic acid encoding mPGES-1, which specifically hybridise with the nucleic acid encoding continuis its expression; (2) a method of inhibiting the expression of mPGES-1 in cells or tissues; and (3) a method of treating an animal continuis a disease or condition associated with MPGES-1. MPGES-1 chimeric antidiabetic, immunomodulator, cardiant, neuroprotective, antidiabetic, usacotropic, antidiabetic, immunomodulator, and antidiabetic, and can be used as mPGES-1 inhibitors and in gene therapy. The antisense compound to ophthalmological, immunomodulatory and cardiovascular activities, and can be used as mPGES-1 inhibitors and in gene therapy. The antisense compound con the used as mPGES-1 inhibitors and in gene therapy. The antisense compound cor an be used for preparing a composition for treating a disease or condition associated with mPGES-1 e.g., inflammation, Alzheimer's disease, arthritis, diabetes, cancer, ischemia or reperfusion injury, or ophthalmic, immunological, cardiovascular or neurological disorder.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        chimeric; antisense oligonucleotide; phosphorothioate; human; microsomal prostaglandin E2 synthase; mPGES-1; mPGES-1 inhibitor; microsomal prostaglandin E2 synthase; imPGES-1; mPGES-1 inhibitor; inhibitor; cardiand; surucparotective; antiinflammatory; neuroprotective; antiinflammatory; neuroprotective; antiinflammatory; immunomodulatory; cardiovascular; gene therapy; inflammation; Alzheimer: disease; arthritis; diabetes; cancer; ischaemia; reperfusion injury; ophthalmic disorder; immunological disorder; cardiovascular disorder; neurological disorder;
                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "phosphorothioate linkages and all cytidine residues are 5-methylcytidines"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human mPGES-1 chimeric antisense oligonucleotide SEQ ID NO:1158.
                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                            0.4%; Score 16.8; DB 1; Length 20;
                                                                                                                                                                                                                                                                                                                                                              Score 10.0.

Pred. No. 1e+03;

Tred. no. 1e+03;

Tred. no. 1e+03;
                                                                                                                                                                                                                                                                                                                               Sequence 20 BP; 8 A; 9 C; 3 G; 0 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /*tag= c
/mod base= OTHER
/note= "2'-O-methoxyethyls"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "2'-0-methocyethyls"
                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
Claim 4; SEQ ID NO 1147; 132pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                          2324 TGTGTGTGTGTGTGTGTG 2343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /mod_base= OTHER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /*tag= a
/mod_base= OTHER
                                                                                                                                                                                                                                                                                                                                                                                                                                                        20 rerererececercierere 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADM14971 standard; DNA; 20 BP
                                                                                                                                                                                                                                                                                                                                                                           90.06;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-JUL-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                            18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16. .20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /*tag=
                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
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modified_base
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  modified base
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADM14971;
                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                            Matches
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The present sequence represents a chimeric antisense oligonucleotide targeted to human microsomal prostaglandin E2 synthase (mPGES-1). The human mPGES-1 gene is located on chromosome 9, more specifically to operate invention also describes: (1) antisense compounds, having a sequence comprising 8-30 bp targeted to a nucleic acid encoding mPGES-1, which specifically hybridise with the nucleic acid encoding inhibits its expression; (2) a method of inhibiting the expression of mPGES-1 in cells or tissues; and (3) a method of treating an animal having a disease or condition associated with mPGES-1. MPGES-1 chimeric antisense oligonucleotides and antisense compounds have cytostatic, antisidabetic, immunomodulator, cardiant, neuroprotective, antiinflammatory, neuroprotective, nootropic, antianthalmological, immunomodulatory and cardiovascular activities, and can be used as mPGES-1 inhibitors and in gene therapy. The antisense compound can be used for preparing a composition for treating a disease or condition associated with mPGES-1 e.g., inflammation, Altheimer's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             disease, arthritis, diabetes, cancer, ischaemia or reperfusion injury, or ophthalmic, immunological, cardiovascular or neurological disorder.
                                                                                                                                                                                                                                                                                                                    New antisense compound, having a sequence targeted to a nucleic acid encoding mPGES-1, useful for preparing a composition for treating e.g., inflammation, Alzheimer's disease, arthritis, diabetes, cancer or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; se; interleukin-4 receptor; ID-4; interleukin-5 receptor; IL-5; CCR1; CCR4; W.CM4; VCDM; LTyptase a; tryptase b; PDE4 A; PDE4 B; PDE4 C; PDE4 D; respiratory disease; tryptase; hyper-responsiveness; adenosine; adenosine A receptor; asthma; lung allergy; inflammation; inflammation; offlammatory disease; airway inflammation; allergy; impeded respiration; cystic fibrosis; CF; chronic observactive pulmonary disease; CCP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     acute respiratory distress syndrome; pulmonary hypertension;
lung inflammation; bronchitis; airway obstruction; bronchoconstriction.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0.4%; Score 16.8; DB 1; Length 20; 0.0%; Pred. No. 1e+03; ve 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 20 BP; 8 A; 9 C; 3 G; 0 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 4; SEQ ID NO 1158; 132pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2325 GTGTGTGTGTGTGTGT 2344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20 Gréréréccédréreren 1
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25-SEP-2003; 2003WO-US030374
                                                               25-SEP-2002; 2002US-0413549P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human oligonucleotide #1684.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          90.06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15-JUL-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 90.0
Matches 18; Conservative
                                                                                                                              (PHAA ) PHARMACIA CORP
                                                                                                                                                                                                                                                            WPI; 2004-305094/28.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens.
                                                                                                                                                                                             Gierse JK;
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                                                                                                                                                                                                                                                                                                                                                                                                                       ischemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 809
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADO46318/
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JS2004049022-A1

WO2004028458-A2

08-APR-2004

11-MAR-2004

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The invention relates to a compound targeted to a nucleic acid molecule encoding the human ABCCS polypeptide. The compound is an antisense oligonucleotide that specifically hybridises with the nucleic acid and inhibite expression of the polypeptide. The antisense oligonucleotide comprises at least one modified internucleoside linkage i.e. a phosphorothioate linkage, at least one modified sugar molety, preferably a 2'-O-methoxyethyl sugar molety, or at least one modified nucleobase comprising a 5-methylcytosine. The antisense compounds are useful for modulating the expression of the human ABCCS polypeptide and in preparation of a composition for trreating hyperproliferative disorders, e.g. cancer. This sequence repersents an antisense oligonucleotide targeted to DNA encoding the human ABCCS polypeptide of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human, ABCC5; ss; antisense oligonucleotide; phosphorothioate linkage;
2'-0-methoxyethyl sugar moiety; 5-methylcytosine;
hyperproliferative disorder; cancer; cytostatic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            New oligonucleotide compound that inhibits expression of ABCC5, useful for preparing a composition for treating hyperproliferative disorder,
Human; ABCC5; ss; antisense oligonucleotide; phosphorothioate linkage;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0.4%; Score 16.8; DB 1; Length 20; 0.0%; Pred. No. 1e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2;
                          2'-O-methoxyethyl sugar moiety; 5-methylcytosine;
hyperproliferative disorder; cancer; cytostatic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 20 BP; 3 A; 9 C; 1 G; 7 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 15; SEQ ID NO 53; 57pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2691 TITCCCACTICCCACCTGC 2710
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                                                                                                                                                                                                                                12-DEC-2002; 2002US-00319893.
                                                                                                                                                                                                                                                                             12-DEC-2002; 2002US-00319893
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       90.06;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 0.4
Best Local Similarity 90.0
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                        (ISIS-) ISIS PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2004-449386/42.
                                                                                                                                        JS2004115649-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                e.g., cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sapiens
                                                                                               Homo sapiens
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                                                                                                                                                                                     17-JUN-2004
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                                                                                                                                                                                                                                                                                                                                                                        Dobie KW;
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ADP44502/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to oligonucleotides anti-sense to an initiation codon, coding region, 5' or 3' intron-exon junction, intron or region with 2-10 nucleotides of the 5'-end or 3'-end of a nucleic acid target chosen from a gene encoding interleukin (IL) -4 receptor, interleukin (IL) -5 receptor, CCR1, CCR3, Ectanial, RANTES, MCP4, CD23, ICAM, VCAM, tryptase a, tryptase b, PDB4 A, PDB4 B, PDB4 C or PDB4 D. The invention also relates to a method of screening a candidate compound that binds to one or more nucleic acid target(s) or expressed product(s), for the prevention and/or treatment of a respiratory or lung disease. The coligonucleotides are useful for reducing or inhibiting expression of a gene or mRNA encoding interleukin -4 receptor, interleukin-5 receptor, CCR1, CCR3, Botaxin-1, RANTES, MCP4, CD23, ICAM, tryptase a, tryptase b, PDB4 B, PDB4 C, or PDB4 D. The oligonucleotides are useful for preventing or treating a respiratory or lung disease. The respiratory or lung disease is associated with hyper-responsiveness to and/or increased levels of adenosine A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel single or multiple target oligonucleotide anti-sense to e.g. initiation codon, intron of respiratory disease-relevant gene e.g. CCR1, RANTES, MCP4, useful for prophylaxis or treating respiratory disease e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          receptor(ë), and/or asthma and/or lung allergies associated with inflammation or an inflammatory disease. The respiratory or lung disease is chosen from airway inflammation, allergy, asthma, impeded respiration, cystic fibrosis (FF), chronic obstructive pulmonary disease (COPD), allergic rhinitis, acute respiratory distress syndrome, pulmonary hypertension, lung inflammation, bronchitis, airway obstruction or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     bronchoconstriction. This sequence represents an oligonucleotide of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 16.8; DB 1; Length 20;
Pred. No. 1e+03;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                Aguilar D, Miller S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Seguence 20 BP; 3 A; 7 C; 5 G; 5 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human ABCC5 DNA antisense oligonucleotide #43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 2; SEQ ID NO 1685; 174pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1886 TCAAGCTGCTGAAGGAGGGC 1905
                                                                                                                                                                                                                                                                                                                                                   Sandrasagra A, Tang L,
n S, Lu H, Cong H;
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                            25-JUL-2003; 2003US-00627930
                                                                     23-APR-2002; 2002WO-US013135
23-APR-2002; 2002WO-US013143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 90.0%;
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADP44427 standard; DNA; 20
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                                                                                                                                                                                     TANG L.
AGUILAR D.
MILLER S.
SHAHABUDDIN S.
                                                                                                                                          NYCE J W.
SANDRASAGRA A.
                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2004-293804/27.
                                                                                                                                                                                                                                                                                                                                                                        Shahabuddin S,
                                                                                                                                                                                                                                                                                                        CONG H.
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                                                                                                                                        (NYCE/)
(SAND/)
                                                                                                                                                                                                                                  (MILL/)
(SHAH/)
(LUHH/)
                                                                                                                                                                                                                                                                                                        (CONG/)
                                                                                                                                                                                                             (AGUI/)
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ADP44427
XX
AC ADP44442
AC ADP4442
DT 09-SEP-
XX
XX
XX
XX
XX
XX
XX
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Human, ds; cytochrome P450 A1; CYP4501A1; UGT2B4; MDR1;

Cytochrome P450 A2; CYP4501A2; cytochrome P450 02E; CYP45002E1; LTF;

Cytochrome P450 A2; CYP4501A2; cytochrome P450 02E; CYP45002E1; LTF;

Cytochrome P450 A2; CYP4501A2; cytochrome P450 02E; CYP45002E1; LTF;

Cytochrome P450 A2; CYP4501A2; dynamical ARNT; cathepsin S; CTS3;

Cyclooxgenase 2; COX2; diazepam binding inhibitor; DBI; haematological;

Cyclooxgenase 2; COX2; diazepam incotensiferase activating protein; FLAP;

Cyclooxgenase 2; COX2; diazepam incotense activatinase thermolabile; STM;

Cyclooxgenase 2; NQO2; sulfotransferase 187;

Cyclooxgenase 2; NQO2; sulfotransferase 2B7;

Cyclooxgenase 2; NQO2; sulfotransferase 2B7;

Cyclooxgenase 2; NQO2; sulfotransferase 2B7;

Cyclooxgenase 2; NQO2; cyclooxgenase receptor;

Cyclooxgenase 2; NQO2; cyclooxgenase receptor;

Cyclooxgenase 2; NQO2; cyclooxgenase 2B7;

Cyclooxgenase 2; NQO2; cyclooxgenase receptor;

Cyclooxgenase 2; NQO2; cyclooxgenase 2B7;

Cyclooxgenase 2B7;

Cyclooxgenase 2; NQO2; cyclooxgenase 2B7;

Cyclooxgenase 2B7;

Cyclooxgenas
                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to a compound targeted to a nucleic acid molecule encoding the human ABCCS polypeptide. The compound is an antisense oligonucleotide that specifically hybridises with the nucleic acid and inhibite expression of the polypeptide. The antisense oligonucleotide comprises at least one modified internucleoside linkage i.e. a phosphorothioate linkage, at least one modified sugar moiety, preferably a 2'-0-methoxyethyl sugar moiety, or at least one modified nucleobase comprising a 5-methylyrosine. The antisense compounds are useful for modulating the expression of the human ABCCS polypeptide and in preparation of a composition for treating hyperproliferative disorders, e.g. cancer. This sequence reperseants a human ABCCS DNA antisense oligonucleotide target region of the invention.
                                                                                                                                                                                                          New oligonucleotide compound that inhibits expression of ABCC5, usefu
for preparing a composition for treating hyperproliferative disorder,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human acetyl choline muscarinic receptor 3 polymorphic sequence #9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0.4%; Score 16.8; DB 1; Length 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    90.0%; Pred. No. 1e+03;
tive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 20 BP; 7 A; 1 C; 9 G; 3 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                   Example 15; SEQ ID NO 128; 57pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2691 TITCCCACTICCCACCTGC 2710
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20 rirrccacriccacacrec 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABS98543 standard; DNA; 21 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 90.0
Matches 18; Conservative
                            (ISIS-) ISIS PHARM INC.
                                                                                                                                              WPI; 2004-449386/42
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                                                                                                                                                                                                                                                                          e.g., cancer
                                                                                     Dobie KW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABS98543;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 812
ABS98543
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Gaps

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This invention relates to the sequence of an isolated nucleic acid
molecule comprising at least one base variation from that of a known
human cytochrome P450 A1 (CYP4501A1), cytochrome P450 A2 (CYP4501A2),
cytochrome P450 O2E1 (CYP45002E1), adrenergic receptor beta1 (ADBR1),
contain (ARBP), cathapsin S (CTSS), cytochromes 2 (COX2), diazapam binding
cytochrome P450 O2E1 (CYP45002E1), adrenergic receptor (BRIZ), bistamine-N-methyl
cransferase (HNMT), NADBH quinone-S-transferase 12 (GYT12), histamine-N-methyl
cransferase (HNMT), NADBH quinone-S-transferase 2 (EMC2),
culfoctansferase (HNMT), NADBH quinone-S-transferase 2 (EMC2),
culfortansferase 2 (EMC2), NADBH quinone-S-transferase 2 (EMC2
                                                                                                                                                                 Isolated nucleic acid molecules having polymorphisms in known human genes eg. cytochrome p450 and cathepsin S useful as genetic linkage markers for locating, identifying and characterizing the genes responsible for disorder-related traits.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       polymorphic DNA sequence of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0.4%; Score 16.8; DB 1; Length 21; 0.0%; Pred. No. 1.1e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cross-linking oligomer 220 for targetting human TNF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 21 BP; 9 A; 0 C; 2 G; 10 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
                                                                                                                                                                                                                                                                                 Example 28; Page 159; 714pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3463 TATATATATCTATATATA 3482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 TATATATGTGTATATATA 21
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28-NOV-2000; 2000US-00724389.
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Best Local Similarity 90.0
Matches 18; Conservative
                                           (DNAS-) DNA SCI LAB INC
                                                                                                                             WPI; 2002-698522/75.
                                                                                 Hall J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAQ20038;
                                                                                    Guida M,
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TD AAQ20
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AC AAQ20
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DT 01-AI
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DB Cross
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28-NOV-2001; 2001WO-US044838.

25-JUL-2002.

Homo sapiens

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Synthetic.

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The sequence is designed to target the Human tumour necrosis factor beginning at nucleotide 1137 and to covalently cross-link to it via the N4N4-ethanocytosine group. See also AAQ20031-Q20037
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tumour necrosis factor; herpes simplex; AIDS; modified; HIV; RSV; HPV; malignancy; hepatitis; inflammation; ss.
                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Oligomer TNF217 for forming triplex with HUMTNFAA target duplex.
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/mod_base= OTHER
/note= "OTHER= N6 methyl-8-oxo-2' deoxyadenine"
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/mod_base= OTHER
/note= "OTHER= N6 methyl-8-oxo-2' deoxyadenine"
21
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/mod_base= OTHER
/note= "OTHER= N6 methyl-8-oxo-2' deoxyadenine"
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/mod_base= OTHER
/note= "OTHER= N6 methyl-8-oxo-2' deoxyadenine"
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/note= "OTHER= N6 methyl-8-oxo-2' deoxyadenine"
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/mod_base= OTHER
/note= "OTHER= N6 methyl-8-oxo-2' deoxyadenine"
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/mod_base= OTHER
/note= "OTHER= N6 methyl-8-oxo-2' deoxyadenine"
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/note= "OTHER= N6 methyl-8-oxo-2' deoxyadenine"
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                                                                                                                                                    Query Match 0.4%; Score 16.8; DB 1; Length 21; Best Local Similarity 90.0%; Pred. No. 1.1e+03; Matches 18; Conservative 0; Mismatches 2; Indels
                                                                                                         Seguence 21 BP; 10 A; 1 C; 0 G; 10 T; 0 U; 0 Other;
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/mod_base= OTHER
/note= "OTHER= N6 methyl-8-oxo-2'
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                                                                                                                                                                                                                                                   3467 TATATCTATATATATATT 3486
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/mod_base= OTHER
/note= "OTHER= N6
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(first entry)
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modified_base
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07-DEC-1992
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                                                                                                                                                                                                                                                                                                   셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HARRING TO THE TOTAL TOT
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                                   deoxyribonucleic acid; major groove, ethanoamino group;
aziridinylcytosine; cross-linking group; tumour necrosis factor; ss.
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/mod_base= OTHER
/note= "N-methyl-8-oxo-2'-deoxyadenine"
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mod_base= OTHER
'note= "N-methyl-8-oxo-2'-deoxyadenine"
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/mod_base= OTHER
/note= "N-methyl-8-oxo-2'-deoxyadenine"
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/mod_base= OTHER
/note= "N-methyl-8-oxo-2'-deoxyadenine"
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/mod_base= OTHER
/note= "N-methyl-8-oxo-2"-deoxyadenine"
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/mod_base= OTHER
/note= "N-methyl-8-oxo-2'-deoxyadenine"
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/note= "N-methyl-8-oxo-2'-deoxyadenine"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'note= "N-methyl-8-oxo-2'-deoxyadenine'
                                                                                                                                                                                                                                                         'note= "N4N4-ethanocytosine"
                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 4; Page 25; 42pp; English
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mod_base= OTHER
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mod_base= OTHER
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/mod base= OTHER
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/mod base= OTHER
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91US-00640654.
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modified_base
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14-JAN-1991;
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deoxyadenine"

vivlemore401-10.rng

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'note= "OTHER= N4 N4 ethanocytosine"
                             /mod_base= OTHER
/note= "OTHER= N6 methyl-8-oxo-2'
                                                          /*tag=
                    *tag=
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08-APR-1991;
17-APR-1991;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23-NOV-1990
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Froehler B,
  ö
                                                                                                                                                                                                                                                                                                   The synthetic oligomer is capable of forming a triplex at physiological pH with a purine rich target sequence by coupling into the major groove of the duplex. The specific target sequence of this oligomer is the human tumour necrosis factor beginning at nucleotide 1137 contg. a purine rich sequence concd. on one strand of the duplex. The oligomer, and others like it are useful in diagnosis and therappy of diseases characterised by specific DNA duplex targets, e.g. HPV, HBR; HIV, hepatitis B, herpes, malignant tumours and inflammation. The triple helices form under mild conditions thus assays may be carried out without subjecting the test specimen to harsh conditions. See also AAQ25452-25501 and AAQ30226-448s. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tumour necrosis factor; herpes simplex; AIDS; modified; HIV; RSV; HPV; malignancy; hepatitis; inflammation; 88.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                          New oligomers contg. modified bases - which form a triplex with G-C doublet in a DNA duplex, for treating and diagnosing HIV, hepatitis, herpes malignancy and inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Oligomer TNF220 for forming triplex with HUMTNFAA target duplex.
/*tag= k
/mod_base= OTHER
/note= "OTHER= N6 methyl-8-oxo-2' deoxyadenine"
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Match 0.4%; Score 16.8; DB 1; Length 21; Local Similarity 90.0%; Pred. No. 1.1e+03; les 18; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                   Matteucci MD, Milligan J;
                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 21 BP; 11 A; 0 C; 0 G; 10 T; 0 U; 0 Other;
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/mod_base= OTHER
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910S-00643382.
910S-00683420.
910S-00686544.
910S-00686545.
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                                                                              91WO-US008811
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(first entry)
                                                                                                                                                                                                     Froehler B, Krawczyk S,
                                                                                                                                                                                 (GILE-) GILEAD SCI INC.
                                                                                                                                                                                                                         WPI; 1992-217083/26,
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modified_base
                                                                                                            18-JAN-1991;
08-APR-1991;
17-APR-1991;
17-APR-1991;
17-APR-1991;
27-SEP-1991;
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07-DEC-1992
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Matches
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The synthetic oligomer is capable of forming a triplex at physiological pH with a purine rich target sequence by coupling into the major groove of the duplex. The specific target sequence of this oligomer is the human tumour necrosis factor beginning at nucleotide 1137 contg. a purine rich sequence concd. on one strand of the duplex. The oligomer, and others
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/mod_base= OTHER
/note= "OTHER= N6 methyl-8-oxo-2' deoxyadenine"
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/mod_base= OTHER
/note= "OTHER= N6 methyl-8-oxo-2' deoxyadenine"
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/mod_base= OTHER
/note= "OTHER= N6 methyl-8-oxo-2' deoxyadenine"
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/note= "OTHER= N6 methyl-8-oxo-2' deoxyadenine"
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/mod_base= OTHER
/note= "OTHER= N6 methyl-8-oxo-2'
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/mod_base= OTHER
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91US-00643382.
91US-00683420.
91US-00686544.
91US-00686546.
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(first entry)

(revised)

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Polymerase chain reaction; PCR; amplify; primer; bi-lateral schwannoma; sequence-tagged site assay; chromosome 22; NT2; deletion; hearing loss; neurofibromatosis; merlin; mossin-erzin-radixin-like protein; D22S28; tumour suppressor; activity; meningioma; cytoskeleton; gene therapy; merlin-associated tumour; D22S1; posterior capsular lens opacity; deafness; balance disorder; paralysis; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                 The tumour suppressor gene merlin - for treatment and diagnosis tumours and neurofibromatosis (NF2).
                                                                         Primer #1 for preparation of merlin cDNA, bases 824-2100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Page 14; 86pp; English.
                                                                                                                                                                                                                                                                                                                                                         (GEHO ) GEN HOSPITAL CORP.
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                                                                                                                                                                                                                                                                                                                                                                                  Trofatter JA,
                                                                                                                                                                                                                                                                    25-FEB-1994;
                                    25-MAR-2003
                                                                                                                                                                                                                                                                                             25-FEB-1993;
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                                                  19-APR-1995
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                                                                                                                                                                                           Synthetic.
           AAQ71073;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA and polypeptide(s) from a new type of hepatitis C virus (KHCV) - for diagnosing and vaccinating against KHCV infections.
 are useful in diagnosis and therapy of diseases characterised by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The sequence is that of PCR primer DA17PSHCV used in the cloning of the 3'-end region of the Korean hepatitis C virus genome. The DNA sequence obtd. was KHCV 266 contg. two terminator codons but no poly(A) tail. (Updated on 25-MAR-2003 to correct PN field.)
          specific DNA duplex targets, e.g. HPV; HER; HIV, hepatitis B, herpes, malignant tumours and inflammation. The triple helices form under mild conditions thus assays may be carried out without subjecting the test specimen to harsh conditions. See also AAQ25452-25501 and AAQ30226-448. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kim CH;
                                                                                                            Match 0.4%; Score 16.8; DB 1; Length 21; Local Similarity 90.0%; Pred. No. 1.1e+03; les 18; Conservative 0; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                    Korean hepatitis C virus; polymerase chain reaction; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              So HS,
                                                                                                                                                                                                                                                                                                                                            KHCV cDNA 3'-end region cloning PCR primer DA17PSHCV
                                                                                     Seguence 21 BP; 10 A; 1 C; 0 G; 10 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 21 BP; 4 A; 3 C; 9 G; 5 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Choi DY,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lim KJ,
                                                                                                                                                                 3467 TATATCTATATATATATTT 3486
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91KR-00013601.
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                                                                                                                                                                                                                                                         21
                                                                                                                                                                                                                                                                                                                    (first entry)
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Best Local Similarity 90.0
                                                                                                                                                                                                                                                        AAQ33326 standard; DNA;
                                                                                                                                                                                                                                                                                                       (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1993-001883/01.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lee YB,
Yang JY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (LUCK-) LUCKY LID.
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19-MAY-1993
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Kim ST,
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Matches
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Gusella JF;

Maccollin MM,

93US-00022034. 93US-00026063. 93US-00108808. 93US-00171718.

94EP-00301367.

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                         regions of the merlin gene. NF2 is a neurofibromatosis which is characterised by bi-lateral schwannomas. The NF2 "gene" has been shown by linkage studies to be assigned to chromosome 22. The missing or mutated
The sequences given in AAQ71073-76 are primers which were used to amplify
                                                                                                             denotes a protein, merlin (moesin-erzin-radixin-like protein), which encodes a protein, merlin (moesin-erzin-radixin-like protein), which possesses tumour suppressor activity, and whose tumour suppressor activity, and whose tumour suppressor possesses tumour suppressor. The merlin gene is found on chromosome 22 between the known markers D2281 and D22828. The merlin gene may be used in gene therapy for the treatment of a merlin-associated tumour or NF2, or for prevention of schwannoma, meningioma, posterior capsular lens opacities, deafness or hearing loss, balance disorders or paralysis. (Updated on 25-MAR-2003 to correct PN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 21 BP; 4 A; 8 C; 5 G; 4 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1614 CATCCACAGGGACCTGGCTG 1633
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04-NOV-1994
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Gaps

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2; Indels

0; Mismatches

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AAQ71073/c ID AAQ71073 standard; DNA; 21

RESULT 817

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WO9504068-A1.
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                              misc_feature
 Synthetic
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AAZ26593
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                                                                                                                                                                                                                                                                                                                                                                                                       The sequences given in AAQ61825-50 and AAQ61886-906 are oligonucleotides which contain a q4 or two q3 stretches and which may be used for inhibiting replication of herpes simplex virus (HSV). Oligonucleotides such as these may also be used for inhibiting activity of HIV, human cytomegalovirus or influenza virus, or for treating inflammatory and neurological disorders caused by phospholipase AZ activity in cases of hyperproliferation, malignancy, cardiovascular disease and snake bite. They may also be used for inhibiting division of malignant cells by modualting telomere length, which may also retard aging. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                          New modified oligo-nucleotide contg guanine quartet - inhibits activity of viruses, e.g. HIV, and phospholipase A2 and modulates telomere length
                                        human cytomegalovirus; influenza virus; inflammation;
neurological disorders; phospholipase A2 activity; hyperproliferation;
malignancy; cardiovascular dadiasese; snake bite; malignancy;
telomere length; retard; agdiss ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Peptide nucleic acid; PNA; HIV; human immunodeficiency virus; AIDS; antiviral; antisense; triple helix; ss.
                                                                                                                                                                                                                                                                                    Chiang M, Brown-Driver VL;
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    /*tag= a
    /note= "Phosphorothionate intersugar linkages"

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                              Inhibition; replication; herpes simplex virus; HSV; HIV;
         HSV replication inhibiting oligomer, ISIS no 4560.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Peptide nucleic acid oligomer targetting HIV gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 21 BP; 0 A; 4 C; 17 G; 0 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                     P, Bennett CF, Chian
Wyatt JR, Imbach JL;
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                                                                                                                     Location/Qualifiers
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Best Local Similarity 90.0
Matches 18; Conservative
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J, Vickers TA, W
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                                                                                                                                                                                                                                                                                                                                                                chromosomes.
                                                                                                                  Key
misc_feature
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19-OCT-1995
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of naturally occurring nucleobases covalently bound to a polyamide backbone and (b) hybridise to the translation initiation AUG region, 5' untranslated region (3' UTR), splice untranslated region (3' UTR), splice junctions or coding sequence of a human immunodeficiency virus gene chosen from env, gag, pol, rev and tat. The PNAs can be used to trarget RNA and single stranded DNA (8sDNA) to produce antisense type gene regulation moieties. They have utility as gene-targetted drugs for modulating HIV processes. Hence they can be used to treat AIDS and other viral infections. They are also useful in diagnostic applications and as created bulk. They are also useful in diagnostic applications and as stranded DNA. They are also useful in diagnostic applications and as treanded DNA. They are also able to form triple helices in which a first PNA strand binds with RNA or ssDNA and a second PNA strand binds with the first PNA strand binds with the first PNA strand binds with the first C resulting double helix or with the first PNA strand binds with a second significant charge and are water soluble, which facilitates cellular uptake. Further, since they contain amides of non-biological amino acids, they are abjoated and resistant to enzymatic degradation by proteases.
                                                                                           /*tag= a
floote= "at least one (and preferably all) of the backbone
shounts are composed of N-acetyl N-(2-aminoethyl)glycine
peptide residues, the nucleobase being attached
covalently to the acetyl group and the peptide linkage
being formed by condensation of the glycine carboxy group
of one residue with the amino group of the 2-aminoethyl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present sequence is a specifically claimed PNA sequence (represented by the sequence of nucleobases) targetting HIV genes. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Oligomer hybridisable to HIV sequence and contg. peptide nucleic acid sub:unit - binds in complementary manner to DNA and RNA, and useful for modulating HIV viral activity, e.g. in treating AIDS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            peptide nucleic acid (PNA) oligomers are provided which (a) consist
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 21 BP; 0 A; 4 C; 17 G; 0 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                              moiety in the next residue"
cocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2920 GGGCGGGCGTGGGGGGCG 2939
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Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (ISIS-) ISIS PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1995-082179/11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
wes 18; Conserv
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kinase gene; protein phosphatase; P450; steroid receptor; cadherin;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 This invention describes a novel method for identifying an inhibitor potentially useful for treatment of cancer, where the inhibitor is active on a gene vital for cell growth or viability, and where the gene is subject to loss of heterozygosity (LOH) in a cancer. The inhibitor is used for preventing the development of cancer in a patient having a precancerous condition, by administering to the patient a first allele specific inhibitor (ASI) targeted to an allele of a first essential gene present in cells of the precancerous condition, where the normal somatic cells of the patient are heterozygous for the first gene, the inhibitor is active on at least one but less than all allelic forms present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            present in a population and targets only one allelic form present in the normal somatic cells, and the first gene. The products and methods can be used in the diagnosis, prevention and treatment of LOH disorders, e.g. cancers, atherosclerotic plaques, premalignant metaplastic or dysplastic lesions, benign tumours, endometriosis, polycystic kidney disease, and graft versus host disease. The method can also be used to remove malignant cells from bone marrow transplants. AAZ25812-Z28825 represent human polymorphic sites described in the method of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Genetic proximity, gene expression, cell characterisation, homeobox gene; genetic defect, reverse transcriptase polymerase chain reaction; RT-PCR;
                            Polymorphism; human; inhibitor; cancer; treatment; cell growth; LOH; cell viability; loss of heterozygosity; precancerous condition; ASI; allele specific inhibitor; somatic cell; diagnosis; prevention; atherosclerotic plaque; premalignant metaplastic lesion; endometriosis; dysplastic lesion; benign tumour; polycystic kidney disease; transplant; graft versus host disease; malignant cell removal; bone marrow; ss.
                                                                                                                                                                                                                                                                                                                                                                Identifying target genes for allele-specific drugs - used for diagnosis, prevention and treatment of, e.g. cancers, atherosclerotic plaque, dysplastic lesions, endometriosis or graft versus host disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0.4%; Score 16.8; DB 1; Length 21; 90.0%; Pred. No. 1.1e+03;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 21 BP; 3 A; 8 C; 8 G; 2 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
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                                                                                                                                                                                                                                                                                                          Stanton VP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1517 CCTGCAAGCCGCCCGAGGAG 1536
                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Fig 7; 605pp; English
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AAZ18215/c
ID AAZ18215 standard; DNA; 21 BP.
  Human polymorphic region 782.
                                                                                                                                                                                                                       98WO-US005419.
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                                                                                                                                                                                                                                                                               (VARI-) VARIAGENICS INC
                                                                                                                                                                                                                                                                                                          Housman D, Ledley FD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                                      WPI; 1998-521232/44.
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                                                                                                                                     Homo sapiens
                                                                                                                                                              WO9841648-A2
                                                                                                                                                                                                                       19-MAR-1998;
                                                                                                                                                                                                                                                  20-MAR-1997;
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The invention provides a new method for identifying and characterising cells. The method for determining the genetic proximity of a first cell and a second cell comprises: (a) obtaining the first cell and the second cell; (b) determining in the first cell and the second cell; (b) determining in the first cell and the second cell; (b) determining the second cell the pattern of expression of genes in a selected gene family; and (c) calculating a proximity index using a specified formula. The methods can be used for caracterising cells, e.g. for determining the origin of a cell; its genetic status, whether it carries a genetic defect, or whether it is transformed. They can be used for detecting a selected genetic defect in ceffect of a selected treatment on a test cell. They can also be used for obtaining cells capable of expressing an homeobox related desired property. The method uses reverse transcriptase polymerase chain reaction containing the pattern of gene expression in a selected gene family. Sequences Asiles of gene expression in a selected in the RT-PCR reactions to determine the pattern of gene expression. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  genes, kinase genes,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Identifying and characterizing cells by comparing the pattern of gene expression in a selected gene family.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0.4%; Score 16.8; DB 1; Length 21; 00.0%; Pred. No. 1.1e+03; ve 0; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Arteriosclerosis-detecting probe from HNF1 #2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity 90.0%; Pred. No. 1.16
nes 18; Conservative 0; Mismatches
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98IL-00126627.
                                                                                                                                                                                                                                                                                                  98WO-IL000625.
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P-PSDB; AAY14749.
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                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                  29-DEC-1997;
16-OCT-1998;
                                                                                                                                                                                                                                                                                                  28-DEC-1998;
                                                                                                                                                                  WO9934016-A2
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                                                                                                                                                                                                                                  08-JUL-1999
primer; sa
                                                               Synthetic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Vider B;
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Matches
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The invention relates to amplifying an unknown region that flanks a known region of a cancer-associated DNA sequence comprising providing a center-associated DNA sequence comprising providing a cemplate bolymucleotide, ligating a loop-forming oligonucleotide to the 3'-end of the sense strand, annealing the loop-forming oligonucleotide with the first portion to generate a panhandle structure, subjecting the panhandle structure to extension, and subjecting the panhandle structure to extension, and subjecting the panhandle structure to extension, and subjecting the method of a cancer-comprised DNA sequence, the template polymucleotide comprises a sense strand, comprising the known and unknown region of a cancer-comprised DNA sequence, the template polymucleotide comprises a first or second portion. The lunknown region is complementary to the sense strand than is the known region. The hoop-forming oligonucleotide is complementary to the first portion. The third region of comprises ATP1 (not defined) or the first portion. The method is useful for amplifying an unknown region that flanks a known region of a cancer-associated DNA sequence. Also disclosed as new is the use of the method in the analysis of the breakpoint regions with AF-4, CDK-6 and SEPTING and are associated With ALL and AML (acute lymphoblastic leukaemia and acute myeloid leukaemia). MLL is located on chromosome the unknown region adjacent to the BCR cancer gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cytostatic; Antiinflammatory; Immunosuppressive; Antibacterial; Virucide; cancer; inflammatory; immune; ds; human secreted protein.
                                                                                                                                                                                                                                                                                                 Amplifying an unknown region that flanks a known region of a cancerassociated DNA sequence by subjecting the panhandle structure to extension and to PCR in the presence of a first primer homologous to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0.4%; Score 16.8; DB 1; Length 21; 90.0%; Pred. No. 1.1e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human secreted protein encoding sequence SEQ ID #1166.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 21 BP; 3 A; 5 C; 7 G; 6 T; 0 U; 0 Other;
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                                                                                                                                                                                                            Rappaport E;
                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 6; Page 42; 80pp; English.
97US-0038624P.
97US-0056938P.
97US-0065911P.
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                                                                       98US-00026033
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Matches 18; Conservative
                                                                                                                                                                                                         Felix CA, Jones DH,
                                                                                                                                       (JONE/) JONES D H. (RAPP/) RAPPAPORT E.
                                                                                                                                                                                                                                                      WPI; 2003-606415/57.
                                                                                                                 (FELI/) FELIX C A. (JONE/) JONES D H.
                                                                                                                                                                                                                                                                                                                                                                      second portion.
                          25-AUG-1997;
17-NOV-1997;
                                                                       19-FEB-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADP29168;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       This invention describes a novel method for determining the genetic risk of arteriosclerosis both for clinical diagnosis and for population studies. The method comprises: (i) selecting risk-associated reference nucleic acid sequences, including their functionally characterizing mutations; (ii) applying probes from these sequences, or their complements, to a carrier, (iii) hybridising the probes with a nucleic acid from (or synthesised from) a patient sample, and (iv) detecting and evaluating the hybridisation pattern. The method provides a quick, in expensive and informative diagnosis, and makes possible a quick, in mutations or mutations that when present alone carry no risk but are risk mutations or mutations that when present alone carry no risk but are risk associated in presence of other mutations. The results may be combined with known risk-assessment methods to provide a more reliable diagnosis, especially important with new therapeutic methods (e.g. gene therapy) that are directed against specific genes. All relevant mutations in a reference sequence can be screened for in a single test and the method is vell mutations the combined for in a single test and the method is vell mutations.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; 88; MLL; cancer; AP-4; CDK-6; SEPTIN6; ALL;
acute lymphoblastic leukaemia; AML; acute myeloid leukaemia;
chromosomal break point; chromosome 11q23; ATF; BCR; B cell receptor;
                                                                                                                                                                                                                                                                                                                      Determining genetic risk of arteriosclerosis, for clinical diagnosis, comprises hybridizing patient nucleic acid with an array of probes derived from risk-associated reference genes and their mutations.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0.4%; Score 16.8; DB 1; Length 21; 90.0%; Pred. No. 1.1e+03; ve 0; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 21 BP; 2 A; 12 C; 7 G; 0 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            illustrate the method of the invention
                                                                                                                                                                                                                                                                                                                                                                                                              Example 1; Page 126; 146pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2909 GGCATGGCCCTGGGCGGGC 2928
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21 GGCCTGGCCCTGGGGGGGC 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              09-APR-2002; 2002US-00118783
                                                                                            13-MAR-2002; 2002WO-EP002780
                                                                                                                                         13-MAR-2001; 2001DE-01011925
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    90.08;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 90.0
Matches 18; Conservative
                                                                                                                                                                                                                                 Seedorf U;
                                                                                                                                                                                                                                                                            WPI; 2002-723374/78
                                                                                                                                                                                    (OGHA-) OGHAM GMBH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US2003096255-A1
    WO200272882-A2
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                                                 19-SEP-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          primer, PCR
                                                                                                                                                                                                                               Cullen P,
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WO2004035732-A2 29-APR-2004

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New nucleic acid molecule for diagnosing, preventing or treating diseases such as proliferative (e.g. cancer), inflammatory, immune, metabolic, genetic, bacterial and viral diseases.
                                                                                                                                                                                                                                                                                                                               The present invention relates to an isolated nucleic acid molecule encoding a polypeptide which is believed to be cytostatic, antiinflammatory, immunosuppressive, antibacterial and virucidal. The composition and methods are useful for diagnosing, preventing and irreating diseases such as proliferative (e.g. cancer), inflammatory, immune, metabolic, genetic, bacterial and viral diseases. The sequence represents a human secreted protein encoding sequence. The present sequence is available on WIPOWEB and is not in the specification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             human; T-cell associated disease; Wheta; autoimmune disease; degenerative nervous system disease; graft versus host disease; hypersensitivity disease; infectious disease; neoplastic disease; degenerative nervous system disease; multiple sclerosis; Alzheimer's disease; hypersensitivity disease; type I hypersensitivity disease; type I hypersensitivity; Goodpasture's syndrome; allergy; type II hypersensitivity; Goodpasture's syndrome; HIV; fungal infection; Candida; parasitic infection; schistosome; filaria; bacterial infection; Mycobacterium; neoplastic disease; lymphoproliferative disease; leukaemia; lymphoma; cancer; brain cancer;
                                                                            Williams LT, Chu K, Lee E, Hestir K, Beaurang PA, Behrens D;
Halenbeck RF, Huang MM, Kothakota S, Haishan L, Linnemann T;
Pierce K, Wang Y, Wong JGP, Wu G, Zhang H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0.4%; Score 16.8; DB 1; Length 21; 90.0%; Pred. No. 1.18+03; tive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 21 BP; 4 A; 1 C; 15 G; 1 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                    Claim 1; SEQ ID NO 1166; 428pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human Vbeta gene repeat sequence #349.
                                          (FIVE-) FIVE PRIME THERAPEUTICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     853 GAGGAGGAGCTGGTGGAGGC 872
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95US-00531241.
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08-AUG-2003; 2003US-0493577P.
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Best Local Similarity 90.0
Matches 18; Conservative
                                                                                                                                                                        WPI; 2004-348438/32.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          JS2002150891-A1
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18-APR-2003; 2002US-0411111P.
18-APR-2003; 2003US-0463700P.
18-APR-2003; 2003US-0463700P.
18-APR-2003; 2003US-0463716P.
18-APR-2003; 2003US-0463732P.
02-MAY-2003; 2003US-0467201P.
02-MAY-2003; 2003US-0467201P.
02-MAY-2003; 2003US-0467201P.
19-MAY-2003; 2003US-047336P.
19-MAY-2003; 2003US-047336P.
22-MAY-2003; 2003US-0471336P.
22-MAY-2003; 2003US-0471336P.
09-JUN-2003; 2003US-0476609P.
09-JUN-2003; 2003US-0476609P.
09-JUL-2003; 2003US-0485218P.
08-JUL-2003; 2003US-0485218P.
                                                                                                                                  29-AUG-2002; 2002US-0406576P.
29-AUG-2002; 2002US-0406599P.
29-AUG-2002; 2002US-0406589P.
29-AUG-2002; 2002US-0406688P.
29-AUG-2002; 2002US-0406688P.
29-AUG-2002; 2002US-0406611P.
29-AUG-2002; 2002US-0406611P.
29-AUG-2002; 2002US-0406612P.
29-AUG-2002; 2002US-0406612P.
29-AUG-2002; 2002US-0406640P.
29-AUG-2002; 2002US-0406640P.
29-AUG-2002; 2002US-0406653P.
29-AUG-2002; 2002US-0406653P.
29-AUG-2002; 2002US-0410946P.
17-SEP-2002; 2002US-0410948P.
17-SEP-2002; 2002US-0410948P.
17-SEP-2002; 2002US-0410948P.
17-SEP-2002; 2002US-0410957P.
17-SEP-2002; 2002US-0410957P.
17-SEP-2002; 2002US-0410957P.
17-SEP-2002; 2002US-0410957P.
17-SEP-2002; 2002US-0410957P.
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17-SEP-2002; 2002US-0411022P.

17-SEP-2002; 2002US-0411024P.

17-SEP-2002; 2002US-0411024P.

17-SEP-2002; 2002US-0411034P.

17-SEP-2002; 2002US-0411035P.

17-SEP-2002; 2002US-0411037P.

17-SEP-2002; 2002US-0411047P.

17-SEP-2002; 2002US-0411045P.

17-SEP-2002; 2002US-0411045P.
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17-SEP-2002; 2002US-0411052P.
17-SEP-2002; 2002US-0411055P.
17-SEP-2002; 2002US-0411073P.
17-SEP-2002; 2002US-0411082P.
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08-AUG-2003; 2003US-0493370P-
08-AUG-2003; 2003US-0493573P-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17-SEP-2002; 2002US-0410959P.
17-SEP-2002; 2002US-0410960P.
17-SEP-2002; 2002US-0410961P.
17-SEP-2002; 2002US-0410962P.
                                                                                              28-AUG-2003; 2003WO-US026780
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Sallberg M,
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                                                                                                                                                                The invention relates to a kit for diagnosing and treating T-cell associated diseases which comprises a panel of nucleic acid primers especifically priming and allowing amplification of each Vbeta gene, VbetaRNA or cDNA. The kit is useful for diagnosing organ transplant redection and diagnosing and treating T-cell associated diseases including autoimmune disease, Appersensitivity disease, infectious diseases including autoimmune disease, Autoimmune diseases include Addison's disease, and neoplastic disease. Autoimmune diseases include Addison's disease, and neoplastic disease. Autoimmune diseases include Addison's disease, arrophic gastritis. Degenerative nervous system diseases include multiple atrophic gastritis. Degenerative nervous system diseases include Type I hypersensitivities such as those present in allergies. Type II hypersensitivities such as those present in cologasture's syndrome and Type IV hypersensitivities such as those caused by arrases such as HUY, fungal infections such as those caused by the yeast genus Candida, parasitic infections such as those caused by Mycobacterium. Neoplastic diseases include lymphoproliferative diseases such as leukaemias, lymphomas and cancers such as cancer of the brain, breast. The present sequence represents a Vbeta gene repeat sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                          Kit for diagnozing and treating T-cell associated diseases e.g. autoimmune, degenerative nervous system and infectious disease, comprises nucleic acid primers specifically priming and allowing amplification of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IL-12 p40 subunit; treatment; intracellular infection; mammal;
immunogenic portion; antigen; intracellular pathogen;
bacterial infection; legionella; tuberculosis; chlamydia;
parastic infection; rickettella; leshmaniasis; malaria; viral infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 22 BP; 9 A; 0 C; 2 G; 11 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PCR primer used to amplify the IL-12 p40 subunit.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
                                                                                                                                       Disclosure; SEQ ID NO 753; 164pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3463 TATATATATATATATATA 3482
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 TATATATGTATATGTATA 21
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les 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (CHIR ) CHIRON CORP.
(SCRI ) SCRIPPS RES INST.
                           WPI; 2004-059052/06
 Rowen L;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO9812332-A1
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                                                                                                           Wheta gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
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 Hood LE,
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                                                                                                                                                     Vector construct directing expression of intracellular pathogenic antigen - useful for, e.g. treatment of intracellular diseases in animals such as tuberculosis and chlamydia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hepatitis B; hepatitis C; immunogen; HBV; HCV; hepatocellular carcinoma; HCC; gene therapy; virucide; hepatotropic; antiinflammatory; cytostatic; PCR primer; human; peripheral blood mononucleocyte; PBMC; interleukin-12; IL-12 p40 subunit; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         viral infections like Hepatitis, Herpes, HIV and FIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 22 BP; 7 A; 6 C; 6 G; 3 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                    Example 2; Page 45; 141pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1820 TCCTGCTCTGGGAGATCTTC 1839
Lee WTL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20 TCTTGCTCTGGGAGATCTGC 1
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93US-00032385.
93US-00102132.
94US-00286829.
95US-00374414.
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Best Local Similarity 90.0
Matches 18; Conservative
Milich DR,
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                                                                               WPI; 1998-217270/19
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04-AUG-1993;
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AAD21248/C
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AC
AAD2124
XX
AC
AAD2124
XX
DT
XX
DE
HUMAN E
XX
HCC; price
HC; price
HC
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Gaps

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WPI; 2002-247917/30.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
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ABLL54523,
ID ABLL54523,
XXX ABLL
DT 27-1
DT
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Sequence 22 BP; 5 A; 8 C; 8 G; 1 T; 0 U; 0 Other;

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Treating hepatitis C infections in a warm-blooded animal by administering a vector construct, which directs the expression of an immunogenic portion of a hepatitis C antigen, and alternatively, with an
                                                                                                                                                                                                                                                                                                                                                                Hepatitis B virus; hepatitis C virus; hepatitis C infection; poliovirus; hepatitis B infection; hepatitis C antigen; polyprotein antigen; SV40; hinovirus; pox virus; avaccinia virus; influenza virus; adenovirus; adenovirus; adenovirus; adenovirus; herpes virus; measles; corona virus; HIV; human immunodeficiency virus; Sindbis virus; IL-2; ss; interfleukira-2; immunomodulatory offactor B7; encephalomyocarditis virus; immunomodulatory ocfactor GR-GSF; IRSS; internal ribosome entry site; virus; virus; hepatotropic; retroviral vector; cytokine; PCR; primer; human.
Score 16.8; DB 1; Length 22;
Pred. No. 1.1e+03;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Townsend K,
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                                                                                  1140 CGAGCTCGAGCTGCCG 1159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lee WTL,
                                                                                                          22 CGCGCTCGAGCTGCCTGCTG 3
                                                                                                                                                                                                                                                                                                                                      Human IL-2 cDNA PCR primer #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   92US-00830417.
93US-00032385.
93US-00102132.
94US-00286829.
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                          90.06;
                                                                                                                                                                                                                     ABX80081 standard; DNA; 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            immunomodulatory cofactor.
                                                                                                                                                                                                                                                                                                22-APR-2003 (first entry)
        Query Match
Best Local Similarity 90.0
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chang SMW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        JOLLY D J.
CHANG S M W.
LEE W T L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2003-174125/17.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens.
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07-JUN-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         04-FEB-1992;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Jolly DJ,
                                                                                                                                                                                                                                                              ABX80081;
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(CHAN/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (ODEA/)
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                                                                                                                                                                                   RESULT 829
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to a gene sequence encoding 23S rRNA of Pectinatus cerevisiphilus (ABL54507). The invention includes a series of oligomucleotide probes including: a sequence (ABL54508-ABL54519) targeting 23S rRNA of a Pectinatus genus microbe for detecting P. cerevisiphilus or its complementary sequence, a sequence (ABL54520-ABL54531) targeting 23S rDNA and 23S rRNA of a Pectinatus genus microbe for detecting P. frisingensis or its complementary sequence; a sequence (ABL54532-ABL54540) targeting 23S rDNA and 23S rRNA of a Pectinatus genus microbe for detecting a Pectinatus genus microbe. The method can be used for detecting a Pectinatus genus microbe. The
                                                                                  The present invention relates to a method for treating hepatitis B or C infections. The method involves administering a vector construct that directs the expression of at least one immunogenic portion of hepatitis B virus (HBV) antigen, containing HBeAg, HbcAg, HbsAg, S, Pre-S1, Pre-S2, open reading frame (ORF) S, ORF 6, HBV pol or HBxAg or co-expression of at least one immunogenic portion of a HBV antigen and at least one immunogenic portion of a hepatitis (HCV) antigen. The vectors are useful in gene therapy, particularly for treating or preventing hepatitis B and hepatitis C infections, as well as hepatocellular carcinomas (HCC). The present sequence is a PCR primer used for amplifying IL-12 (interleukin-12) p40 subunit of human peripheral blood mononucleocytes (PBMC) used in the exemplification of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pectinatus bacteria in beer, from the microbes.
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0
                                                                                                                                                                                                                                                                                                                                                                                 Length 22;
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Pred. No. 1.1e+03;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pectinatus frisingensi 23S rRNA probe SEQ ID NO 17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pectinatus; 23S rRNA; Pectinatus cerevisiphilus;
                                                                                                                                                                                                                                                                                                                                            Sequence 22 BP; 7 A; 6 C; 6 G; 3 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pectinatus frisingensis; beer; probe; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A nucleic acid probe for detecting detection of nucleic acids derived
                                                                                                                                                                                                                                                                                                                                                                                                                                                             1820 TCCTGCTCTGGGAGATCTTC 1839
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 3; Page 11; 14pp; Japanese
                                                      Example 2; Col 29; 64pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20 rcriecrcressadarcrec 1
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                                                                                                                                                                                                                                                                                                                                                                                   0.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
              hepatocellular carcinomas.
                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity 90.0
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Gaps

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Indels Length

22;

Score 16.8; DB 1; Pred. No. 1.1e+03; 0; Mismatches

0.4%;

1820 TCCTGCTCTGGGAGATCTTC 1839

20 rcriecrcreseadarcrec 1

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AAF29247 standard; DNA; 23

vivlemore401-10.rng

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Query Match
Best Local Similarity 90.0
Matches 18; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to a method for treating intracellular infections within warm-blooded animals comprising administering to a warm-blooded animals wethin warm-blooded animals are according to a manal and a vector construct which directs the expression of at least one immunogenic portion of an antigen derived from an intracellular pathogen, an immunogenic portion of the antigen to generate an immune response. The method is useful for treating intracellular infections or diseases including viral infections (e.g. hepatitis B virus (HBV), hepatitis C virus (HIV) or feline immunodeficiency virus (FIV)), parasitic infections (e.g. rickettsia, leishmaniasis or malaria) and certain bacterial diseases (e.g. legionella, tuberculosis or chlamydia). Sequences ABX96883-ABX96937 and ABX96940-ABX96965 represent PCR primers used in the method of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Treating intracellular infections, e.g. viral, parasitic and bacterial diseases, comprises administering a vector construct which directs the expression of an immunogenic portion of an antigen from an intracellular
Sindbis virus. This sequence represents a PCR primer used in the method of the invention
                                                                                                                                                                             Gaps
                                                                                                                                                                                ö
                                                                                                                        Length 22;
                                                                                                                      Query Match 0.4%; Score 16.8; DB 1; Length 2
Best Local Similarity 90.0%; Pred. No. 1.1e+03; J
Matches 18; Conservative 0; Mismatches 2; Indels
                                                                            Sequence 22 BP; 7 A; 6 C; 6 G; 3 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Interleukin-12 (IL-12) DNA PCR primer #1.
                                                                                                                                                                                                                            1820 TCCTGCTCTGGGAGATCTTC 1839
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 2; Page 18; 69pp; English
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                                                                                                                                                                                                                                                                    20 TCTTGCTCTGGGAGATCTGC 1
                                                                                                                                                                                                                                                                                                                                                                                                          BP
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                                                                                                                                                                                                                                                                                                                                                                                                          ABX96942 standard; DNA;
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MILICH D R.
LEE W T L.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15-MAY-2003
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ABX96947/C

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99US-0143536P.

13-JUL-1999;

Antibody; platelet factor 4; heparin; PF4/heparin complex; mouse; HIT; heparin induced thrombocytopaenia; heparin induced thrombosis; HITT;

PCR primer; KKO; ss.

WO200104159-A1.

18-JAN-2001

Mus musculus.

PCR primer for amplification of antibody KKO H chain V region cDNA.

(first entry)

17-APR-2001

AAF29247;

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This invention relates to a composition comprising a monoclonal antibody which binds specifically with a Platelet Factor 4 (PP4)/heparin complex. The antibody preferentially binds to the complex relative to the binding of the antibody with either of the components alone. Methods are included for the production of the antibody and its use in the diagnosis of various diseases. The composition can be used for diagnosing heparin induced thrombocytopaenia/thrombosis, HIT/HITT: The composition can also be used for assessing the level of a polyclonal antibody that binds specifically within a bodily fluid or tissue sample. The present sequence represents a PCR primer used to amplify cDNA encoding the variable region of the heavy chain of the antibody of the invention which is referred to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                  Composition for the diagnosis and treatment of heparin induced thrombocytopenia/thrombosis, comprises an antibody that preferentially binds with a Platelet Factor 4/heparin complex.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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Pred. No. 1.2e+03;
1; Mismatches 3; Indels
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                                                           ŝ
                                                           Kamei K, Kamei
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(SCTE-) SCI & TECHNOLOGY CORP @UNM
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                                                                                                                                                                                                                                                                                                                      Example 1; Page 47; 80pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 GAGGTGAAGCTGGTGGAGWCWG
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Best Local Similarity 81.8%;
Matches 18; Conservative
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                                                           Kisiel W,
                                                                                                                          WPI; 2001-138321/14.
                                                           Arepally G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 832
AAC83856
ID AAC8389
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Seguence 22 BP; 7 A; 6 C; 6 G; 3 T; 0 U; 0 Other;

99EP-00201558

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(TARG-) TARGET QUEST BV.
                                            Hoogenboom HRJM;
        18-MAY-1999;
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                                                                                                                                                                                                                                                                                          Matches
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                                                                                                                                                                                                                                                                                        The present invention relates to a human Fab fragment library. The Fab fragment library is useful for selecting an antigen-binding Fab using in vitro selection on immobilised or labelled antigen such as monoclonal Fab or polyclonal collection of Fab clones that specifically bind to MUC1. The obtained antibodies are useful as research reagents or as therapeutic products and also are important for target validation and target valuable source of functional genomics. The Fab library is a valuable source of antibodies for many different targets, and is useful to screen off-rates for a large series of the antigen specific Fabs. The present sequence is a PCR primer used to construct the Fab library of the
                                                                                                                                                                                                                                   Phage display libraries of human Fab fragments useful for isolating high-affinity antibodies against specific target comprises polynucleotides encoding CDR containing domains of heavy chain and light chain genes.
                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; Fab fragment; antigen-binding; antibody; PCR primer; ss
                                                                Human; Fab fragment; antigen-binding; antibody; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                         0.4%; Score 16.8; DB 1; Length 23; 81.8%; Pred. No. 1.2e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                             3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 23 BP; 3 A; 3 C; 12 G; 3 T; 0 U; 2 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                             1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                853 GAGGAGGAGCTGGTGGAGGCTG 874
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GAGGTGCAGCTGGTGGAGWCYG 22
                                                                                                                                                                                                                                                                          Disclosure, Fig 2; 74pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99EP-00201558.
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                                                                                                                                                            99EP-00201558
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                            (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                              (TARG-) TARGET QUEST BV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VH back PCR primer #4.
                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
es 18; Conserva
                                                                                                                                                                                                                   WPI; 2001-042369/06.
                                                                                                                                                                                                 Hoogenboom HRJM;
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                                                                                                                                                             18-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EP1054018-A1
                                                                                                                                         18-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     02-MAR-2001
                             02-MAR-2001
                                                                                    Homo sapiens
                                                                                                      EP1054018-A1
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                                                                                                                        22-NOV-2000.
                                                VH back PCR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAC83855;
                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
         AAC83856;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 833
                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
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                                                                                                                                                                                                                                          The present invention relates to a human Fab fragment library. The Fab fragment library is useful for selecting an antigen-binding Fab using in vitro selection on immobilised or labelled antigen such as monoclonal Fab or polyclonal collection of Fab clones that specifically bind to MUC1. The obtained antibodies are useful as research reagents or as therapeutic products and also are important for target validation and target valuable source of functional genomics. The Fab library is a valuable source of antibodies for many different targets, and is useful to screen off-rates for a large series of the antigen specific Fabs. The present sequence is a PCR primer used to construct the Fab library of the
                                                  Phage display libraries of human Fab fragments useful for isolating high-affinity antibodies against specific target comprises polynucleotides encoding CDR containing domains of heavy chain and light chain genes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Identifying toxicologically relevant canine gene to determine toxicological responses of agents, by obtaining and comparing gene expression profiles of untreated canine cells and canine cells treated with an agent.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Left PCR primer used to target prostaglandin D synthase canine
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0.4%; Score 16.8; DB 1; Length 23; 81.8%; Pred. No. 1.2e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 23 BP; 3 A; 3 C; 11 G; 5 T; 0 U; 1 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Canine gene array; toxicological response; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Dunn RT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (PHAS-) PHASE-1 MOLECULAR TOXICOLOGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 853 GAGGAGGAGCTGGTGGAGGCTG 874
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 5; Page 52; 140pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Fig 2; 74pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABL99446 standard; DNA; 23 BP
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WPI; 2001-042369/06.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             present invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABL99446;
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Sequence 23 BP; 5 A; 4 C; 9 G; 5 T; 0 U; 0 Other;

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gene and the generation of an array of toxicologically relevant canine genes. The gene array is useful for obtaining a gene expression profile, by exposing a population of cells to an agent, obtaining cDNA from the population of cells, labeling the cDNA, and contacting the CDNA with the gene array. The relevant gene is useful for making and using arrays to determine toxicological responses to various agents, and also useful for identifying novel gene sequences and novel canine genes. The method for analysing toxicological responses using the canine gene array is rapid and efficient. The present sequence is related to the canine gene array
This invention relates to identifying a toxicologically relevant canine
                                                                                                                                                                                                                                                                                                                                                                                Sequence 23 BP; 4 A; 9 C; 5 G; 5 T; 0 U; 0 Other;
886666666666888888
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Gaps ; 0 0.4%; Score 16.8; DB 1; Length 23; 00.0%; Pred. No. 1.2e+03; 2; Indels 0; Mismatches 1040 AGGIGICCCIGGAGICCAAC 1059 18; Conservative Best Local Similarity Matches 18; Conserv Query Match ઠે

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1 AGGTGTCCTGCAGCCCAAC 20

ACF06327 standard; DNA; 23 ACF06327;

BP

07-OCT-2003 (first entry)

Zebrafish vasa PCR primer SEQ ID NO:3.

Zebrafish; fish embryo cell line; chimeric fish; genetic; human disease; vasa; PCR primer; ss

Danio rerio. Synthetic. WO2003051109-A1.

26-JUN-2003.

.3-DEC-2002; 2002WO-US039913

13-DEC-2001; 2001US-0341355P. 12-FEB-2002; 2002CA-02371460.

(PURD) PURDUE RES FOUND.

Collodi P, Fan L, Ma

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WPI; 2003-532958/50.

New zebrafish embryo cell line, which becomes a germ cell when introduced to a fish embryo, useful for making a germ line chimeric zebrafish, which is a valuable model for genetic studies of human diseases.

Example 2; Page 23; 45pp; English.

The present invention describes a fish embryo cell line, where a cell of the fish embryo cell line, after incubation in vitro for at least 24 devours, will become a germ cell when introduced to a fish embryo. Also described: (1) making the fish embryo cell line; (2) an isolated fish embryo cell line obtained by the method of (1); (3) making a germ line chimeric fish; (4) a germ line chimeric fish obtained by the method of (3); and (5) cell culture media comprising a growth factor and fish cell conditioned medium, or a growth factor and a fish cell conditioned medium, or a growth factor and a fish cell in a fish germ line chimeric fish, particularly zebrafish, which is a valuable model for genetic studies of human diseases. The present sequence represents a PCR primer for zebrafish vasa, which is used in an example from the present invention

BP.

ACF05339 standard; DNA; 23

ACF05339 ID ACF0 XX

RESULT 837

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New isolated polypeptide micro-scaffold displaying immunoglobulin complementarity determining region (CDR) 2 or CDR3 polypeptide sequences, useful for searching, selecting and screening for immunoglobulin CDR2 or CDR3 polypeptide sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to an isolated polypeptide micro-scaffold displaying immunoglobulin complementarity determining region (CDR) -2 or CDR3 polypeptide sequences, comprising a CDR2 or CDR3 polypeptide sequence interconnecting fragments of the adjacent framework polypeptide sequences, which are arranged to form two anti-parallel beta-strands. The polypeptide micro-scaffold and the nucleotide sequences are useful for searching, selecting and screening for immunoglobulin CDR2 or CDR3 polypeptide sequences. The present sequence is a PCR primer used for the primary amplification of human heavy chain variable region (VH)
                                                                                                                                                                                                                                                                                                                            Micro-scaffold; immunoglobulin; complementarity determining region; CDR; human; heavy chain variable region; VH; PCR; primer; 88.
                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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Match 0.4%; Score 16.8; DB 1; Length 23; Local Similarity 90.0%; Pred. No. 1.2e+03; es 18; Conservative 0; Mismatches 2; Indels
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Pred. No. 1.2e+03;
                                                                                                                                                                                                                                                                                            Human VH region amplifying antisense PCR primer, VH3B-Back.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 23 BP; 3 A; 3 C; 11 G; 5 T; 0 U; 1 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             853 GAGGAGGAGCTGGTGGAGGCTG 874
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                                                                    646 GIGGAGGIGAAIGGCAGCAA 665
                                                                                                    2 Greckerckerckerk 21
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Best Local Similarity 81.8%;
Matches 18; Conservative
                                                                                                                                                                                      AAL62076 standard; DNA; 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lasters I, Pletinckx J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (ALGO-) ALGONOMICS NV. (ABLY-) ABLYNX NV.
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                                                                                                                                                                                                                                                          22-SEP-2003
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 Query Match
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                                  Matches
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vivlemore401-10.rng

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The present sequence is that of a PCR primer annealing to framework region 1 of human heavy chain variable region (VH) genes. The primer was used, with an oligo-dT primer, in the amplification of a human donors as template. This provides an example of the method of human donors as template. This provides an example of the method of the invention, which relates to the cloning of immunoglobulin variable of momens (IGVD) and the construction of IGVD expression librariable method involves first strand cDNA synthesis from mRNA using a universal primer, performing second strand cDNA synthesis using a first primer capable of hybridising to a site at, or adjacent to, the 3' end of each of the IGVD sequences on the antisense strand, cleaving the double-stranded DNA with a restriction enzyme to produce double-stranded DNA encoding a functional IGVD fragment, and cloning the resulting variable
                                                                                                                                                                                                                                                                                                                                                                                                      Cloning polynucleotide sequences encoding immunoglobulin variable do (IGVD) for the manufacture of a medicament by cloning the resulting variable domain fragment sequences into a vector.
                                                                                              Antibody; immunoglobulin; variable domain; human; PCR; primer; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0.4%; Score 16.8; DB 1; Length 23; 81.8%; Pred. No. 1.2e+03; ve 1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    human; single nucleotide polymorphism; SNP; ss; primer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 23 BP; 3 A; 3 C; 11 G; 5 T; 0 U; 1 Other;
                                                                                                                                                                                                                                                                                                     (VLAA-) VLAAMS INTERUNIVERSITAIR INST BIOTECHNOG.
                                                                 Human VH gene framework region 1 PCR primer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               encoding a functional IGVD fragment, and domain fragment sequences into a vector
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 3; Page 22; 31pp; English
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                                                                                                                                                                                                                                    20-DEC-2002; 2002WO-EP014662
                                                                                                                                                                                                                                                                     21-DEC-2001; 2001EP-00205100
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les 18; Conservative
                               06-NOV-2003 (first entry)
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                                                                                                                                                                     WO2003054016-A2
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                                                                                                                                                                                                                                                                                                                                        Muyldermans S;
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                                                                                                                                   Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention relates to novel antibody sequences, which acts against lesioned tissue. Also claimed is a method (M1) for isolating polynucleotide encoding the antibodies, which involves (a) isolating B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tsunoda H;
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                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                        Novel polynucleotide useful for PCR amplification along with two DNA fragment from another set of sequences, or for detecting single nucleotide polymorphism in human gene.
                                                                                                                                                                                                                                     The present invention relates to a polynucleotide isolated from a Pagene and is useful for detecting a single nucleotide polymorphism i Muman gene or for diagnosing of disease. The invention enables the detection of a single nucleotide polymorphism in a human gene. The present sequence represents a primer of the invention.
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                                                                                                                                                                                                                                                                                                                                                                   Query Match 0.4%; Score 16.8; DB 1; Length 23; Best Local Similarity 90.0%; Pred. No. 1.2e+03; Matches 18; Conservative 0; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                       Sequence 23 BP; 10 A; 10 C; 1 G; 2 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 3; SEQ ID NO 103; 200pp; Japanese.
                                                                                                                                                                                                            Claim 2; SEQ ID NO 4411; 2627pp; Japanese.
                                                                             (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Antibody related primer, SEQ ID 103.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (CHUS ) CHUGAI SEIYAKU KK.
(PHAR-) PHARMALOGICALS RES PTE LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                     2318 TGTGTGTGTGTGTGCGTG 2337
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               08-MAR-2002; 2002JP-00064373.
                                             08-MAR-2002; 2002JP-00064373.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADP03730 standard; DNA; 23
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                                                                                                             WPI; 2004-093977/10.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         solated B cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO2004048571-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Isuchiya M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10-JUN-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADP03730;
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Gaps

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cells that is infiltrated into lesioned tissue, and (b) acquiring bolynucleotide that encodes an antibody from the isolated B cells. The antibodies are useful for treating cancer lesions, arteriosclerosis, inflammatory disease or autolimmune disease. The present sequence was used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   motife of glycine-rich repeat sequences (GRRS). Full length GRRS sequences, such as the Epstein-Barr virus strain B95.8 nuclear antigen (EBNA1) represented by AAW05704, can be used in the method of the invention is for making an antigenic protein invisible to the immune system, and consists of inserting a GRRS into the antigenic protein. The method can be used to insert a GRRS into the antigenic protein. The method can be used to insert a GRRS into
                                                                                                                                                                                                                                                                                                                                                                                                                                        Glycine-rich repeat sequence; immune system; regulatory protein; enzyme; cytokine; lymphokine; cell adhesion molecule; costimulatory molecule; drug resistance; tumour suppressant; genetic disease; viral disease; enzyme disorder; Gaucher's disease; cancer; immune system disorder; GRNS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New proteins containing GRRS which are invisible to the immune system .
used for treating cancer, immune system disorders, viral diseases, etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAT39966-T39973 represent double stranded coding sequences for minimal
                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                         Epstein-Barr virus; EBV; nuclear antigen; EBVNA1; antigenic protein;
                                                                                                                                                          ö
                                                                                                                                                         3; Indels
                                                                                                                          Score 16.8; DB 1; Length
Pred. No. 1.2e+03;
                                                                                             Sequence 23 BP; 3 A; 3 C; 11 G; 5 T; 0 U; 1 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "5' overhang"
complement(24)
/*tag= b
/note= "5' overhang of TTCC"
                                                                                                                                                       1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                          Minimal motif coding sequence ZGR1/ZGR2
                                                                                                                                                                                       853 GAGGAGCTGGTGGAGGCTG 874
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                       Example 1; Page 43; 61pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gene therapy; minimal motif; ds.
                                                                                                                                                                                                                                                                                                ВР
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    95SE-00001324.
95US-00522995.
95US-00529190.
                                                                                                                            0.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       96WO-GB000876
                                                                to illustrate the invention.
                                                                                                                                                                                                                                                                                               AAT39968 standard; DNA; 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               / rag= a
/note= "5'
                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                         18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1996-477134/47.
                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P-PSDB; AAW05707
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (MASU/) MASUCCI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO9632483-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .0-APR-1996;
                                                                                                                                                                                                                                                                                                                                                            24-JUN-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10-APR-1995,
01-SEP-1995,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17-0CT-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Synthetic
                                                                                                                                                                                                                                                                                                                             AAT39968;
                                                                                                                          Query Match
                                                                                                                                                       Matches
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therapeutic proteins, marker genes, regulatory proteins of viral vectors, or vaccine components. The therapeutic proteins include enzymes, cytokines, lymphokines, cell adhesion molecules, costimulatory molecules, or protein products of drug resistant genes or tumour suppressor genes. The antigenic proteins or corresponding nucleic acids are used to treat genetic and viral diseases, especially enzyme disorders such as Gaucher's disease, cancer, immune system disorders and other diseases treatable by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequences shown in AAV55812 to AAV55827 represent primers used in the course of the invention for the multimerisation of minimal motifs. The invention provides a method for increasing the reasstance of a core protein to protein that comprises linking or inserting onto or into the core protein a stabilising polypeptide of formula (I(Glya)x(Glyb)x(Glyc)Zln where Glya, Glyb, Glyc are 1-6 sequential Gly residues and X, Y, Z are Ala, Ser, Val, Ile, Leu, Met, Phe, Pro or Thr and n can be anything between 1-66. X, Y and Z need not be identical from n repeat to n repeat. Alternatively a nucleic acid encoding a stabilising polypeptide can be linked onto or inserted into a nucleic acid encoding a core protein. The fusion proteins of the invention are more resistant to degradation by proteases and, thus, have a longer half-life than the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New fusion proteins resistant to proteolytic degradation - comprising a core protein with a stabilising polypeptide comprising a peptide sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fusion protein; stabilising polypeptide; proteolytic degradation; resistance; half-life; autoimmune disease; inflammation; nitro drug; lkappab regulator protein; inflammatory bowel disease; in vivo imaging; nitroreductase protein; enzyme therapy; produg therapy; protease; cancer; pathological condition; minimal motif; PCR primer; ss.
                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                               Score 16.8; DB 1; Length 24; Pred. No. 1.2e+03;
                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Multimerisation of minimal motifs using primer ZGE2.
                                                                                                                                                                           Seguence 24 BP; 5 A; 2 C; 14 G; 3 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure, Page 72; 120pp; English
                                                                                                                                                                                                                                                                                         2123
                                                                                                                                                                                                                                                                                                                               24 Accedeacerceascrere s
                                                                                                                                                                                                                                                                                           2104 ACCCCCAGCTCCAGCTCCTC
                                                                                                                                                                                                                                                                                                                                                                                                                               BP.
                                                                                                                                                                                                                 0.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             containing glycine repeats.
                                                                                                                                                                                                                                                                                                                                                                                                                               AAV55819 standard; DNA; 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                           Query Match
Best Local Similarity 90.0
Matches 18; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human herpesvirus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17-NOV-1997;
                                                                                                                                     gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO9822577-A1
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18-NOV-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAV55819;
                                                                                                                                                                                                                                                                                                                                                                                         RESULT 841
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Sequences shown in AAV55812 to AAV55827 represent primers used in the course of the invention for the multimerisation of minimal motifs. The invention provides a method for increasing the resistance of a core protein to proteolytic degradation that comprises linking or inserting onto or into the core protein a stabilising polypeptide of formula [(Glya)X(Glyb)Y(Glyc)Zln where Glya, Glyb, Glyc are 1-6 sequential Gly and n can be anything between 1-66. X, Y and Z need not be identical from n repeat to n repeat. Alternatively a nucleic acid encoding a stabilising polypeptide can be linked onto or inserted into a nucleic acid encoding a core protein. The fusion proteins of the invention are more resistant to degradation by proteases and, thus, have a longer half-life than the unfused core protein? The products can be used for treating autoimmune
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unfused core protein. The products can be used for treating autoimmune diseases, cancer and inflammation. In particular, the core protein may be an IkappaB regulator protein for the treatment of inflammatory bowel disease, or a nitroreductase protein which can activate nitro drugs in enzyme/prodrug therapy to treat cancer or other pathological conditions. The fusion proteins can also be used in diagnostic methods such as in vivo imaging. (Updated on 27-AUG-2003 to correct OS field.)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fusion protein; stabilising polypeptide; proteolytic degradation; resistance; half-life; autoimmune disease; inflammation; nitro drug; IkappaB regularor protein; inflammatory bowel disease; in vivo imaging; nitroreductase protein; enzyme therapy; prodrug therapy; protease; cancer; pathological condition; minimal motif; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                      0.4%; Score 16.8; DB 1; Length 24; 90.0%; Pred. No. 1.2e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                      2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Multimerisation of minimal motifs using primer ZGR1.
                                                                                                                                                                                                                                                                                  Sequence 24 BP; 3 A; 14 C; 2 G; 5 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page 72; 120pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2103 CACCCCCAGCTCCAGCTCCT 2122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4 CACCCGCACCTCCAGCTCCT 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          96US-0030986P.
97US-0048945P.
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                                                                                                                                                                                                                                                                                                                                                                                          90.06;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (revised)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                             18; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
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25-JUN-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         27-AUG-2003
18-NOV-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28-MAY-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Synthetic
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AAV55816/
AAV5816/

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diseases, cancer and inflammation. In particular, the core protein may be an IkappaB regulator protein for the treatment of inflammatory bowel disease, or a nitroreducease protein which can activate nitro drugs in enzyme/prodrug therapy to treat cancer or other pathological conditions. The fusion proteins can also be used in diagnostic methods such as in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Autoimmune regulator; AIR; immune maturation; immune response; disease; autoimmune polyendocrinopathy candidiasis ectodermal dystrophy; APECED; autoimmune polyglandular syndrome type 1; APS I; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    PCR primer GR1/51F used to identify mutations in exon 6 of APECED gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Antonarakis S, Lalioti M;
                                                                                                                                                                                             Gaps
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                                                                                                                                                              24;
                                                                                          vivo imaging. (Updated on 27-AUG-2003 to correct OS field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                               2; Indels
                                                                                                                                                         0.4%; Score 16.8; DB 1; Length 90.0%; Pred. No. 1.2e+03; ive 0; Mismatches 2; Indels
                                                                                                                          Sequence 24 BP; 5 A; 2 C; 14 G; 3 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 24 BP; 6 A; 7 C; 8 G; 3 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Autoimmune regulator 1 (AIR1) DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Scott H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     in the diagnosis and treatment of APECED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LTD.
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                                                                                                                                                                                                                                 2104 ACCCCCAGCTCCAGCTCCTC 2123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 3; Page 13; 59pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (FIIM-) FINNISH IMMUNOTECHNOLOGY
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                                                                                                                                                                                                                                                                24 Accedeacciceaderecte 5
                                                                                                                                                                                                                                                                                                                                                       BP
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Best Local Similarity 90.0
Matches 18; Conservative
                                                                                                                                                                               Local Similarity 90.0
nes 18; Conservative
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Kudoh J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1999-244390/20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO9915559-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                         AAX26955;
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Matches
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This sequence represents a fibronectin inhibitor oligonucleotide. The invention relates to a fibronectin inhibitor protein GBP-1. The GBP-1 protein inhibits the expression of the fibronectin gene. The protein gene can be used to produce antibodies against the GBP-1 protein. The GBP-1 DNA, protein and antibody sequences can be used for the research of expression inhibition of fibronectin in relation to cell growth, cancer and cell aging
                                                                                                                                A DNA coding a protein inhibiting the expression of fibronectin geneused for research of expression inhibition of fibronectin related to cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention relates to a method of amplifying and determining target mutant Ras sequences in a DNA sample, involving the use of a thermostable restriction enzyme and primers shown in AAL47773-AAL47771. The method used is designated restriction mediated selection polymerase chain reaction (REMS-PCR). The method can be used to detect H-ras, K-ras
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Amplifying and determining mutant sequences in DNA sample using thermostable restriction enzyme so that during thermocycling mutant sequences are enriched while wild-type sequences and/or primer induced sites are cleaved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 K-ras; N-ras; H-ras; ras; oncogene; mutation detection; PCR; primer; probe; restriction mediated selection PCR; cancer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 16.8; DB 1; Length 24; Pred. No. 1.2e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 24 BP; 3 A; 4 C; 14 G; 3 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (ORTH ) ORTHO CLINICAL DIAGNOSTICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2928 CGTGGGGGGCGTGGAGGGA 2947
                                                                                                                                                                                                              Disclosure; Fig 8; 21pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; Page 84; 116pp; English.
                                                        8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 CGTGGGGGGGCGGAAGGGA 22
                                                                                                                                                                        growth, cancer and cell ageing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ras gene PCR primer SEQ ID NO:
                                                        (SUME ) SUMITOMO ELECTRIC IND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fuery CJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                          0.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             02-OCT-2001; 2001WO-US042422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 02-OCT-2000; 2000US-0237416P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAL47757 standard; DNA; 24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 90.0 Matches 18; Conservative
                                                                                              WPI; 2000-154339/14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2002-479599/51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200229005-A2
                    06-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unidentified.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18-SEP-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAL47757;
                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This sequence represents a fibronectin inhibitor oligonucleotide. The invention relates to a fibronectin inhibitor protein GBP-1. The GBP-1 protein inhibits the expression of the fibronectin gene. The protein sequence can be used to produce antibodies against the GBP-1 protein. The GBP-1 DNA, protein and antibody sequences can be used for the research of expression inhibition of fibronectin in relation to cell growth, cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A DNA coding a protein inhibiting the expression of fibronectin gene -used for research of expression inhibition of fibronectin related to cell growth, cancer and cell ageing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fibronectin inhibitor; GBP-1; cell growth; cancer; cell aging; 88.
                                                                                                                                                                                                                                                Fibronectin inhibitor, GBP-1, cell growth, cancer, cell aging, ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                                                            Fibronectin inhibitor oligonucleotide #3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fibronectin inhibitor oligonucleotide #6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2928 CGTGGGGGGGCGTGGAGGGA 2947
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 4; Page 13; 21pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (SUME ) SUMITOMO ELECTRIC IND CO
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3 GGCTCCAAGAAGTGCATCCA 22
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                                                                                                                                                                        (first entry)
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es 18; Conservative
                                                                                              AAZ90146 standard; DNA;
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                                                                                                                                                                                                                                                                                          Unidentified
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                                                                                                                                    AAZ90146;
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RESULT 845
AAZ90153
1D AAZ90153
XX AC AAZ901
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XX XX BE FIDEON
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This invention describes a novel nucleic acid containing a specific segment having at least one region that modulates expression of the VR1 (vanilloid receptor, or a functional derivative, allele crafform to this region, or a sequence that hybridises to it under standard conditions. The VR1 modulator is derived from one or more of positions 22191-223144 of GenBank AL670399, 11673-36159 of AL663116, or 4731-43231 or 36616-33151 of AP166739 and is involved in transmission of pain, particularly in primary sensory neurons. The invention also chescribes a vector that contains the VR1 modulator, host cells containing this vector (other than human germ or embryonal stem cells) and a method for modulating expression of the VR1 receptor by introducing the modulator or the vector into a cell that contains the VR1 gene. The modulator or the intention are used for detecting a transcription factor from its binding to a regulatory sequence (or a double-stranded oligonucleotide fragment of it), e.g. by Western blotting or enzymetre in the binding to a regulatory sequence (or a double-stranded oligonucleotide fragment of it), e.g. by Western blotting or enzymetre from its binding site for a transcription factor, e.g. WZR1, NEARDEBS, NEAT or binding site for a transcription factor, e.g. WZR1, NEARDEBS, NEAT or CATANA. The mucleic acids of the invention, or vectors containing them, are used for prevention or treatment of pain, also for treating sensitivity disorders, e.g. analgesia, hypalgesia or hyperalgesia, also
                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                         ds; VR1 receptor; vanilloid receptor type 1; modulator; pain transmission; primary sensory neuron; transcription factor; detection; MZF1; NFkappaB; NFAT; GATA1; sensitivity disorder; analgesia; hypalgesia; hyperalgesia; neuralgia; myalgia; murine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         nucleic acid that modulates expression of the vanilloid receptor-1, inl for control of pain or sensitivity disorders, comprises sequences
and N-ras mutations, which may lead to cancer. The present sequence is PCR primer useful in the method of the invention
                                                                                                         Gaps
                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                  Murine VR1 exon 1d transcription factor binding fragment #39.
                                                                         Score 16.8; DB 1; Length 24; Pred. No. 1.2e+03;
                                                                                                        2; Indels
                                             Sequence 24 BP; 3 A; 6 C; 10 G; 5 T; 0 U; 0 Other;
                                                                                                        0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          from control regions of the receptor gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Schaefer MKH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Page 49; 68pp; German
                                                                                                                                     834 GCTGGTGGTGCTGCCAGCCG 853
                                                                                                                                                                 s écredrédrédrécrédede 24
                                                                                                                                                                                                                                            ADQ30147 standard; DNA; 24 BP.
                                                                         0.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          09-DEC-2002; 2002DE-01057421
                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                         18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (CHEF ) GRUENENTHAL GMBH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Weihe E, Bieller A,
                                                                            Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO2004053120-A2.
                                                                                                                                                                                                                                                                                                      09-SEP-2004
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                                                                                                                                                                                                                                                                          ADQ30147;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New altered CD40L promoter for use in the study, diagnosis and treatment of a variety of inflammatory disorders and autoimmune diseases, such as rheumatoid arthritis.
neuralgia and myalgia, that are associated with activity of the VR1 receptor. This sequence represents a fragment of murine VR1 exon 1d DNA which is capable of binding to a transcription factor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; CD40L; promoter; CD40 ligand promoter; rheumatoid arthritis; diagnosis; antiarthritic; antirheumatic; immunosuppressive; antiinflammatory; inflammatory disease; autoimmune disease; ds.
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                                                                                                                                                                                                  0.4%; Score 16.8; DB 1; Length 24; 90.0%; Pred. No. 1.2e+03; rive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 29 BP; 22 A; 4 C; 0 G; 3 T; 0 U; 0 Other;
                                                                                                                                      Sequence 24 BP; 13 A; 6 C; 2 G; 3 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (NYRE-) NEW YORK SOC RELIEF RUPTURED & CRIPPLED.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CD40L poly-A tract sequence SEQ ID NO:19.
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                                                                                                                                                                                                                                                                                                                                                                                             21 TTTCTCTAGGATTTTTGTTT 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAF74922 standard; DNA; 29 BP
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                                                                                                                                                                                                                Query Match
Best Local Similarity 90.0
Matches 18; Conservative
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Best Local Similarity
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vivlemore401-10.rng

Hepatitis C virus (HCV) NS5B replicase RNA synthesis template #4.

21-OCT-2002 (first entry)

ABK99274;

Hepatitis C virus; HCV; NS5B replicase; 88; RNA polymerase

06-APR-2001; 2001US-00828034.

JS2002064771-A1 30-MAY-2002.

Synthetic.

07-APR-2000; 2000US-0195852P.

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The present invention relates to an assay system for hepatitis C virus (HCV) replicase activity. The assay system comprises an RNA template that has an unstable, small stemloop at the 3 end capable of forming a copyback structure, a HCV non-structural protein 58 (NS5B), ATP, GTP, CTP, and UTP nucleoside triphosphates (NTPS), where one of the NTP is cailolabelled and an assay buffer that supports replication activity of NS5B. The invention also relates to the identification of optimal properties of an RNA template for copy-back self-priming RNA synthesis of properties of an RNA template for copy-back self-priming RNA synthesis of CT to characterise the biological relevance of lead compounds. The optimal RNA templates can be used for developing a system to characterise optimal RNA templates can be used for developing a system to characterise coptimal RNA molecules to co-crystallise with HCV NSSB polymerase mechanistically and kinetically and for designing small RNA molecules to co-crystallise with HCV NSSB polymerase. The assay system of the invention is useful for detecting HCV replicase activity.

The nucleic acid synthesised by NSSB is detected by evaluating an autoradiograph of reaction products separated by gel electrophoresis. The present sequence is RNA template, '(MU)4 used to direct RNA synthesis by the control of the control o
                                                                                                                                                                                                                    RNA template, (AU)4 used to direct RNA synthesis by HCV RNA polymerase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Assay system for hepatitis C virus replicase activity comprises RNA template with unstable, small stemloop capable of forming copy-back structure, viral non-structural protein 5B, nucleoside triphosphates,
                                                                                                                                                                                                                                                                          HCV replicase; non-structural protein 5B; NS5B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0.4%; Score 16.8; DB 1; Length 36; 66.7%; Pred. No. 1.8e+03; ve 0; Mismatches 12; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               in the exemplification of the invention
                                                                                                                                                                                                                                                                       Hepatitis C virus; HCV replicase; lead compound; RNA polymerase; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 1; Fig 1C; 10pp; English.
                                                        AAD27121 standard; RNA; 36 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99US-00309670.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99US-00309670
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Zhong W, Hong Z, Lau JYN;
                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2002-096587/13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HONG/) HONG Z.
[LAUJ/) LAU J Y N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (ZHON/) ZHONG W. (HONG/) HONG Z.
                                                                                                                                                                                                                                                                                                                                                          Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                US6322966-B1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11-MAY-1999;
                                                                                                                                                              09-APR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27-NOV-2001.
                                                                                                              AAD27121;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         buffer.
RESULT 84
AAD27121/
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Novel replicase complex comprising hepatitis C virus NS5B replicase, a 3 nucleotide-long template to which a 2 nucleotide-long primer is annealed, and template and primer which do not form a stable duplex in the absence

Hong Z, Ferrari E;

Zhong W,

HONG/) HONG Z. (FERR/) FERRARI E. ZHON/) ZHONG W.

WPI; 2002-582330/62.

Example; Page 6; 17pp; English.

of HCV NS5B.

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The invention relates to a replicase complex comprising a hepatitis C virus (HCV) NSSB replicase protein, a linear nucleic acid template and a complementary nucleic acid primer which is annealed to the 3' terminus of the template, where the template is at least three nucleotides and the primer is two or three nucleotides, and the template and primer do not form a stable duplex in solution in the absence of the HCV NSSB protein. The complex is useful for detecting HCV replicase activity and permits establishment of sensitive RNA-dependent RNA polymerase assays to screen and evaluate antiviral inhibitors and to improve the specificity and evaluate antiviral inhibitors and to improve the specificity and cfficacy of the inhibitors. The complex is also useful in the development of a reliable system for determining kinetic and thermodynamic constants of HCV NSSB-catalysed nucleotide incorporation and investigation of mechanistic inhibitors for mas-incorporation and investigation of mechanistic properties of NSSB replication and ultimately in the screening assays which are used for determining kinetic, thermodynamic and mechanistic properties of NSSB replication and ultimately in the development of inhibitors of NSSB. Newly identified inhibitors of ceplicase activity may be used for developing anti-HCV pharmaceuticals. Sequences ABK99271-ABK99296 represent HCV NSSB replicase RNA synthesis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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0
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Pred. No. 1.8e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3464 ATAIAIAICIAIAIAIAIAIAIIAIIAIIGAGIIIIIAC 3499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 36 BP; 29 A; 0 C; 2 G; 0 T; 5 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 36 ATATATATATTTTTTTTTTTTTTTTTTTTTTTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAD27118 standard; RNA; 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            09-APR-2002 (first entry)
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es 24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAD27118;
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Matches
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AAD27118/c
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exaxe
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Gaps

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3464 ATATATATATATATATATATATATATAGATTTTAC 3499

1 Similarity 66.7%; 24; Conservative

Query Match Best Local Similarity

Best Loca Matches

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36

ઠ 셤 RESULT 850 ABK99274/c ID ABK99274 standard; RNA; 36 BP.

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The present invention relates to an assay system for hepatitis C virus (HCV) replicase activity. The assay system comprises an RNA template that has an unstable, small stemloop at the 3' end capable of forming a copyback structure, a HCV non-structural protein 5B (NSSB), ATP, GTP, CTP, and UTP nucleoside triphosphates (WTPS), where one of the NTP is radiolabelled and an assay buffer that supports replication activity of NSSB. The invention also relates to the identification of optimal properties of an RNA template for copy-back self-priming RNA synthesis of HCV. This activity can be used to screen for anti-HCV replicase compounds or to characterise the biological relevance of lead compounds. The coptimal RNA templates can be used for developing a system to characterise (CC NSSB polymerase mechanistically and kinetically and for designing system of the invention is useful for detecting HCV replicase activity. The nucleic acid synthesised by NSSB is detected by evaluating an autoradiograph of reaction products separated by gel electrophoresis. The present sequence is RNA template, (AU) 5 used to direct RNA synthesis by RNA polymerase proteins of HCV, BNUY and polivirus. This sequence is used in the exemplification of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 inter-simple sequence repeat; ISSR; SSR; PCR; primer; genotyping; plant;
             RNA template, (AU)5 used to direct RNA synthesis by HCV RNA polymerase.
                                                                                                                                                                                                                                                                                                                                                                                                                          Assay system for hepatitis C virus replicase activity comprises RNA template with unstable, small stemloop capable of forming copy-back structure, viral non-structural protein 5B, nucleoside triphosphates.
                                                HCV replicase; non-structural protein 5B; NS5B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0.4%; Score 16.8; DB 1; Length 36; 16.7%; Pred. No. 1.8e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3464 ATATATATCTATATATATATTTATTGAGTTTTTAC 3499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 36 BP; 29 A; 0 C; 2 G; 0 T; 5 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
                                                                     lead compound; RNA polymerase; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 1; Fig 1A; 10pp; English.
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U.45;

Best Local Similarity 66.78;
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                                                                                                                                                                                                                                                                                                                                                            Lau JYN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PCR primer 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2002-096587/13.
                                                  Hepatitis C virus;
                                                                                                                                                                                                                                                                                                                                                            Zhong W, Hong Z,
                                                                                                                                                                                                                                                                                                                         LAU JY N.
                                                                                                                                                                                                                                                                                       ZHON/) ZHONG W.
                                                                                                                                                                                                                                                                                                          HONG Z.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ISSR-related
                                                                                                                                                                                                                11-MAY-1999;
                                                                                                                                                                                                                                                     11-MAY-1999;
                                                                                                         Unidentified.
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                                                                                                                                            US6322966-B1
                                                                                                                                                                                27-NOV-2001.
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                                                                                                                                                                                                                                                                                                          (HONG/) 1
(LAUJ/) 1
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AC AL
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New set of inter-simple sequence repeats (ISSR)-PCR primers for genotyping eukaryotes, useful for genotyping diverse genomes of plant and animal systems.
                                                                                                                                                                                                                                                                                                                               The invention relates to a novel set of inter-simple sequence repeats (ISSR)-PCR primers for genotyping eukaryotes. The primers of the invention may be useful for genotyping diverse genomes of plant and animal systems, in particular for distinguishing Basmati rice varieties from non-Basmati rice varieties and traditional Basmati rice varieties from evolved Basmati rice varieties. The current sequence is that of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Polymorphism; biallelic; human; forensic; paternity testing; disease; detection; phenotypic typing; characteristic; infection; hereditary; autoimmune disease; cancer; inflammation; drug; therapy; medicament; treatment; marker; primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0.4%; Score 16.6; DB 1; Length 17;
44.1%; Pred. No. 8.9e+02;
ve 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human biallelic polymorphic marker downstream primer #425.
                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 17 BP; 0 A; 0 C; 8 G; 8 T; 0 U; 1 Other;
                                                                                                                                                                (DNAF-) CENT DNA FINGERPRINTING & DIAGNOSTICS
                                                                                                                                                                                                                                                                                                                                                                                                 from evolved Basmati rice varieties. The ISSR-related PCR primer of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (WHED ) WHITEHEAD INST BIOMEDICAL RES.
                                                                                                                                                                                                                                                                                                      Disclosure; Page 19; 60pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2335 GIGIGIGIGIGIGIG 2351
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 96US-0030455P
                                                                                                            09-JAN-2003; 2003WO-IB000041.
                                                                                                                                    08-APR-2002; 2002IN-CH000260.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  94.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAX10119 standard; DNA; 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16; Conservative
animal; Basmati rice; ss.
                                                                                                                                                                                                                     WPI; 2003-804317/75.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity
                                                     WO2003085133-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       05-NOV-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16-NOV-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO9820165-A2
                           Unidentified.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14-MAY-1998.
                                                                                                                                                                                           Nagaraju JG;
                                                                                  16-0CT-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAX10119;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
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(PLAC ) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN
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                                                                                                                                                                                                                WPI; 1999-478980/40
                                                                                                                                                              PCR primer; ss
                                                                                                                                                                      Homo sapiens
                                                                                                                                                                            WO9937299-A1
                                                                                                                                                                                        22-JAN-1999;
                                                                                                                                                                                              22-JAN-1998;
                                                                                                                                07-0CT-1999
                                                                                                                                                                                  29-JUL-1999
                                                                                                                                                                    Synthetic
                                                                                                                          AAZ00748;
                                                                                     Query Match
                                                                                                                 RESULT 854
                                                                                           Matches
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nvention
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                                                                                                                                                                                                       AAX09121-X10268 are allele-specific oligonucleotide primers used in the isolation of various biallelic polymorphic markers found in the human genome (represented in AAX10269-X12937). These primers can be used in a method for determining polymorphic forms in an individual for use in e.g. forensics, paternity testing or for phenotypic typing for diseases such as agammaglobulinemia, diabeters insipidus, lesch-Nyhan syndrome, muscular dystrophy, Wiskott-Aldrich syndrome, Pabry's disease, familial hypercholesterolemia, polycystic kidney disease, hereditary spherocytosis, von Willebrand's disease, tuberous sclerosis, hereditary spherocytosis, von Willebrand's disease, tuberous sclerosis, hereditary amemorrhagic tealangiacteria, familial colonic polyposis, Ehlers-Danlos syndrome, osteogenesis imperfecta, acute intermittent porphyria, autoimmune diseases, inflammation, cancer, diseases of the nervous system, infection by pathogenic microorganisms, and characteristics such as longevity, appearance (e.g. baldness, obesity), strength, speed, endurance, fertility, and susceptibility or receptivity to particular drugs or therapeutic treatments. The isolated polymorphic nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                New isolated nucleic acid segments from the human genome - used for determining polymorphic forms for use in e.g. forensics, paternity testing or phenotypic typing for disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0.4%; Score 16.6; DB 1; Length 23; 32.6%; Pred. No. 1.2e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 23 BP; 8 A; 1 C; 7 G; 7 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
                                                                                                                                                               Claim 16; Page 202; 310pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         82.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         prophylaxis of such diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity 82.6
les 19; Conservative
WPI; 1998-286974/25.
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0; Mismatches 1009 CACAAGATCTCCCGCTTCCCGCT 1031 23 cágaágcrérecererretri BP 99WO-EP000405. 98DE-01002377. AAZ00750 standard; DNA; 23 (first entry) PCR primer; 88 Homo sapiens. WO9937299-A1 22-JAN-1999; 07-OCT-1999 22-JAN-1998; 29-JUL-1999, Synthetic AAZ00750; RESULT 855 FGFR-4; transmembrane domain; human, fibroblast growth factor receptor; overexpression; cytostatic; receptor tyrosine kinase inhibitor; cancer; kinase inactive; treatment; prophylaxis; tyrosine kinase-related; hyperproliferation; invasion; disease; carcinoma; metastasis; detection; breast cancer; aquamous cell carcinoma; glioblastoma; neuroblastoma; uterine cancer; diagnosis; screening assay; predisposition; mutant; Human FGFR-4 transmembrane domain PCR primer #2. 1354 GAGATGATGAAGATGATCGGGAA 1376 1 GAGATGTTGAAATGTTCTGGAA 23 AAZ00748 standard; DNA; 23 BP (first entry)

Knyazev P;

98DE-01002377.

99WO-EP000405

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                                                                                                                                            the receptor (FGFR)-4, that causes overexpression and/or altered activity of the receptor in calls and has cytostatic activity. The product of the invention is a receptor tyrosine kinase inhibitor. A receptor tyrosine kinase inhibitor, especially mutated FGFR-4 (kinase inactive) is useful for treatment and/or prophylaxis of over functional receptor tyrosine kinase-related conditions, especially cancer. The inhibitor can also be back to disease, particularly carcinoma, particularly through inhibition of metastasis. The inhibitor is used to treat breast cancer, squamous cell carcinoma, glioblastoma, neuroblastoma and/or uterine cancer. Detection of a mutated FGFR-4 or a sequence encoding it, can be used in differential diagnosis of cancer, or in a screening assay to determine a predisposition to developing cancer. This sequence represents a PCR primer used to amplify the FGRF-4 fragment used in the method of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  overexpression; cytostatic; receptor tyrosine kinase inhibitor; cancer; kinase inactive; treatment; prophylaxis; tyrosine kinase-related; hyperproliferation; invasion; disease; carcinoma; metastasis; detection; breast cancer; squamous cell carcinoma; glioblastoma; neuroblastoma; uterine cancer; diagnosis; screening assay; predisposition; mutant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FGFR-4; transmembrane domain; human; fibroblast growth factor receptor;
A mutated fibroblast growth factor receptor 4 overexpressed or having altered activity, useful in diagnosis of cancer cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A mutated fibroblast growth factor receptor 4 overexpressed or having altered activity, useful in diagnosis of cancer cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                            This invention describes a novel mutated fibroblast growth factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 16.6; DB 1; Length 23; Pred. No. 1.2e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 23 BP; 7 A; 2 C; 11 G; 3 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human FGFR-4 transmembrane domain PCR primer #4.
                                                                            Example; Page 16; 51pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example; Page 16; 51pp; German
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 0.4
Best Local Similarity 82.6
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ullrich A, Bange J,
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23;

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receptor (FGFR) - that causes overexpression and/or altered activity of the receptor in cells and has cytostatic activity. The product of the invention is a receptor tyrosine kinase inhibitor. A receptor tyrosine kinase inhibitor. A receptor tyrosine kinase inhibitor, especially mutated FGFR-4 (kinase inactive) is useful for treatment and/or prophylaxis of over functional receptor tyrosine kinase-related conditions, especially cancer. The inhibitor can also be used to treat cancer and/or hyperproliferation and/or invasion that leads back to disease, particularly carcinoma, particularly through inhibition of metastasis. The inhibitor is used to treat breast enacer, squamous cell carcinoma, glioblastoma, neuroblastoma and/or invair.
                                                                                                                                                               cell carcinoma, glioblastoma, neuroblastoma and/or uterine cancer.

Detection of a mutated FGFR-4 or a sequence encoding it, can be used in differential diagnosis of cancer, or in a screening assay to determine a predisposition to developing cancer. This sequence represents a PGR primer used to amplify the FGRF-4 fragment used in the method of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Determining methylation state of FMR1 gene promoter for diagnosing fragile X syndrome in males involves denaturing DNA sample, subjecting DNA to bisulfite modification, amplifying DNA and detecting products.
                                                                                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; FWR1; FWRP; Fragile X syndrome; methylation; diagnosis; chromosome Xq27.3; PCR primer; 88.
                                                                                                                                                                                                                                                                                                                 Score 16.6; DB 1; Length 23; Pred. No. 1.2e+03; 0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human FMR1 gene triplet repeat PCR primer NM-BS-for.
                                                                                                                                                                                                                                                                                       Sequence 23 BP; 7 A; 2 C; 11 G; 3 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                       1009 CACAAGAICTCCCGCTTCCCGCT 1031
                                                                                                                                                                                                                                                                                                                                                                                                               23 CAGAAGCTCTCCCTTCCCTCT
                                                                                                                                                                                                                                                                                                                      0.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAC83579 standard; DNA; 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 82.6
Matches 19; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2001-006432/01.
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                                                                                                                                                                                                                                                          invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAC83579;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New therapeutic vaccine compositions comprising at least one purified recombinant hepatitis C virus (HCV) single or specific oligomeric recombinant envelope protein El or E2, useful for immunizing humans from
                                                                                                                                                                                                                                                                                                            Hepatitis C virus; HCV; El protein; E2 protein; infection; primer; PCR; virucide; immunostimulant; vaccine; ss.
                                   Gaps
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                                   4; Indels
Score 16.6; DB 1; Length
Pred. No. 1.2e+03;
0; Mismatches 4; Indels
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                                                                   GTGTGT 2350
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                                                                                        23 TTTGGGAGTGTGTGTATGTGTGT 1
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   0.4%; Sc.
ilarity 82.6%; Pr.
Conservative 0;
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                                                                                                                                                                                   AAL48953 standard; DNA; 23 BP.
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30-AUG-2001; 2001US-0315768P.
                                                                                                                                                                                                                                                  (first entry)
                                                                     2328 TGTGTGCGTGTGTGTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (INNO-) INNOGENETICS NV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bosman F,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2002-599657/64.
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ses 19; Conserv
                    Local Similarity
ses 19; Conserv
                                                                                                                                                                                                                                                                                                                                                              Hepatitis C virus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HCV infection.
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                                                                                                                                                                                                                  AAL48953;
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Matches
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RESULT 858

The present invention describes a novel method of diagnosing Fragile X syndrome using a PCR-based method of methylation analysis. The FWRI gene promoter. Incated at chromosome XQZ7.3, is composed of a CGG trinucleotide repeat. The expansion of this repeat leads to a premutation and then a full mutation, the latter of which is likely to cause the methylation of a nearby CGG island, causing the Fragile X syndrome phenotype. This method is useful in the design of appropriate therapies and counselling for affected individuals and carriers

Claim 17; Col 31; 20pp; English.

Sequence 23 BP; 11 A; 10 C; 0 G; 2 T; 0 U; 0 Other;

ADD69476/c

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Diagnosing, preventing and treating non-small cell lung cancer (NSCLC) comprises determining an expression level of an NSCLC-associated gene in
                                                                                                                                                                                                                                                                          The invention comprises an Hepatitis C virus (HCV) vaccine for reducing liver disease. The vaccine of the invention comprises an HCV B1 or E2 protein as an antigen. The HCV vaccine is useful for reducing liver disease (e.g. liver fibrosis) in a chronic HCV-infected mammal. The present DNA sequence represents a PCR primer that was used in the exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to a method of diagnosing non-small cell lung cancer (NSCLC) or a predisposition to developing NSCLC in a subject by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                   New hepatitis C virus (HCV) vaccine composition, useful for reducing
liver disease, e.g., liver fibrosis in a chronic HCV-infected mammal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human NSCLC gene semi-quantitative PCR primer forward primer #103
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ss; primer; cytostatic; gene therapy; vaccine;
non-small cell lung cancer; NSCLC; diagnosis; cancer; URLC1.
                                                                                                                                                                                                                                                                                                                                                                                                                                              0.4%; Score 16.6; DB 1; Length 23; 82.6%; Pred. No. 1.2e+03;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                                                                           Example 11; SEQ ID NO 106; 271pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2164 GCCCCACCCAGCAGTGGGGCTC 2186
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23 GCGCTACCCAGCAGCGGGAGCTC 1
                                                                                                           Bosman
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2003US-0451374P.
2003US-0466100P.
               18-DEC-2001; 2001US-00020510.
16-OCT-2002; 2002US-0418358P.
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Best Local Similarity 82.6
Matches 19; Conservative
                                                                      (INNO-) INNOGENETICS NV.
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                                                                                                           Depla E,
                                                                                                                                              WPI; 2003-541632/51.
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28-FEB-2003;
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                                                                                                           Maertens G,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New set of inter-simple sequence repeats (ISSR)-PCR primers for genotyping eukaryotes, useful for genotyping diverse genomes of plant and animal systems.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to a novel set of inter-simple sequence repeats (ISSR)-PCR primers for genotyping eukaryotes. The primers of the invention may be useful for genotyping diverse genomes of plant and animal systems, in particular for distinguishing Basmati rice varieties from non-Basmati rice varieties and traditional Basmati rice varieties from evolved Basmati rice varieties.
                                                                                                                                                           inter-simple sequence repeat; ISSR; SSR; PCR; primer; genotyping; plant; animal; Basmati rice; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hepatitis C virus; HCV; vaccine; liver disease; El protein; E2 protein;
liver fibrosis; ss; PCR; primer.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 23 BP; 10 A; 10 C; 2 G; 1 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3' anchored (ISSR)-PCR primer of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                               (DNAF-) CENT DNA FINGERPRINTING & DIAGNOSTICS
                                                                                                                            3' anchored (ISSR)-PCR primer - SEQ ID 34.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; SEQ ID NO 34; 60pp; English.
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                 ВР
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                                                                                                                                                                                                                                                                                                                                     09-JAN-2003; 2003WO-IB000041
                                                                                                                                                                                                                                                                                                                                                                          08-APR-2002; 2002IN-CH000260
                 DNA; 23
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               ADD69476 standard;
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                                                                                                                                                                                                                      Synthetic
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                          decrease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hepatitis C virus; HCV; El glycoprotein; E2 glycoprotein; HCV infection;
liver disease; liver fibrosis; ss; serum alanine aminotransferase level;
steatosis; anti-E2 immunoreactivity; PCR; primer.
determining the expression level of a NSCLC-associated gene in a biological sample derived from the subject, where an increase or decreas of the level compared to a normal control level of the gene indicates that the subject suffers from or is at risk of developing NSCLC. The method is useful in diagnosing NSCLC or a predisposition to developing NSCLC in a subject. The compound, polymoucleotide and the encoded polypeptide and composition are useful in treating or preventing NSCLC. This sequence corresponds to a primer for semi-quantitative PCR amplification of genes that are differentially expressed in NSCLC cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Use of hepatitis C virus (HCV) vaccine composition for reducing liver disease, serum alanine aminotransferase levels, steatosis, or anti-E2 immunoreactivity in the liver of a chronic HCV-infected mammal.
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                                                                                                                                                                                                                                            Length
                                                                                                                                                                                                   Sequence 23 BP; 6 A; 4 C; 6 G; 7 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                          2972 AGCAGAGGACCAGGGCTTTTTTT 2994
                                                                                                                                                                                                                                                                                                                                               1 AGCAGAGGATCAGAGCTTTCTTT 23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BP.
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16-OCT-2002; 2002US-0418358P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADP71196 standard; DNA; 23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2004-499089/47.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hepatitis C virus
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cc specific oligomeric recombinant El or E2 proteins or its parts and optionally a pharmaceutical adjuvant), a composition (comprising at least cone El or E2 peptide, and optionally, a pharmaceutical adjuvant), an immunogenic HCV composition (or HCV vaccine composition) comprising a recombinant virus allowing expression of at least one HCV recombinant convocation (selected from an E1 protein and/or an E2 protein, and their parts, and optionally, a pharmaceutical adjuvant) and an HCV vaccine composition (comprising a recombinant virus allowing expression of at least one HCV recombinant envelope protein changes from an E1 protein and/or an E2 protein, and parts of the E1 and E2 proteins and, conforming in a cuseful for reducing liver disease (such as liver fibrosis or its progression), serum ALT levels, status in a chronic HCV-infected mammal, or for treating a chronic HCV infected mammal, or for treating a chronic HCV in vitro monitoring HCV disease or prognosing the response to treatment of patients suffering from HCV infection. The present sequence is a PCR primer used in the production of Glycosylation site-deleted mutants of the HCV P1 proteins.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention provides the protein and coding sequences of human ATP dependent membrane conjugated zinc proteinase 10.45. The sequences can be used in the treatment of developmental disturbances and lipid metabolism disease. The present sequence is a PCR primer for the coding sequence of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New polypeptide-human ATP dependent membrane conjugated zinc proteinase 10.45 and polynucleotide for encoding such polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; ATP dependent membrane conjugated zinc proteinase 10.45; enzyme; development disturbance; lipid metabolism disease; gene therapy; PCR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATP dependent membrane conjugated zinc proteinase 10-45 PCR primer #2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                 0.4%; Score 16.6; DB 1; Length 23; 82.6%; Pred. No. 1.2e+03; ive 0; Mismatches 4; Indels
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                                                                                                                                                                                                                                                                                                                                                                                               Sequence 23 BP; 2 A; 8 C; 9 G; 4 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 2; Page 17(Disclosure); 34pp; Chinese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (BODE-) BODE GENE DEV CO LTD SHANGHAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2164 GCCCCACCCAGCAGTGGGGGCTC 2186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23 GCGCTACCCAGCAGCGGGAGCTC 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        05-JUN-2000; 2000CN-00116334.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAL45613 standard; DNA; 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity 82.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2002-206994/27.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens.
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97WO-US012961.

Dale RMK,

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Treating bacterial infections in humans or animals with oligo:nucleotide(s) - resistant to nuclease and targetted to bacterial nucleic acid or proteins, also conjugates of these oligo:nucleotide(s)
                                                                                                                                                                                                  Nuclease resistant antisense oligo NBT 140 targeted against (AT)9.
                                                                                                                                                                                                                                         Nuclease resistant; bacterial infection; antibiotic; target; veterinary medicine; treatment; human; industrial process; bacterial control; 88.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (OLIG-) OLIGOS ETC & OLIGOS THERAPEUTICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 49; Page 87; 163pp; English.
                                               AAV21967 standard; DNA; 18
                                                                                                                                                14-JUL-1998 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            with antibiotics.
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                                                                                                                                                                                                                                                                                                                                                     Synthetic.
                                                                                                 AAV21967;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Arrow A,
RESULT 864
AAV21967
                                                                                                 The sequence is that of a bovine microsatellite sequence obtd. by
screening a library of bovine Mool DNA fragments of between 250 and 500
by with an (AC15 and a (TC15 oligonuclectide probe. One out of 50
clones cross-hybridised. Assuming independent distribution of
microsatellites and Mbol sites, the frequency of (T6)n >9 microsatellites
in the bovine genome is estimated at >100, 000. The sequence information
cross-fication and indexed herein (see below). The sequence upstream and
specification and indexed herein (see below). The sequences upstream and
commercem of the microsatellite sequence were used to generate the
required PCR primers for in vitro amplification of the corresp.
crequired PCR primers for in vitro amplification of the corresp.
microsatellite (using the program OPTIPRIM). The microsatellites may be
used to identify individuals, for parentage testing, and in the genetic
mapping of economic trait losi, or genes involved the determinism of
economically important traits esp. in cattle, to allow selective
breeding. See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 - used in genetic identification, gene
                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage; genetic mapping; traits; amplification; ss.
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                       Length 24;
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                                                                      4; Indels
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                     Score 16.6; DB 1;
Pred. No. 1.3e+03;
0; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Microsatellite sequence from clone TGLA189.
                                                                                                                      2824 ATATATACATATATATATAAC 2846
                                                                                                                                                        24 ATATATATAAATATGTATGTC 2
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                     Query Match 0.4%;
Best Local Similarity 82.6%;
Matches 19; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                       (revised)
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02-FEB-1993
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                                                                                                                                                                                                                                                                                                                                                     AAQ33786;
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AM033786

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AM AMO3786

DDT 02-F-M
DDT 02-F-M
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This antisense oligonucleotide is nuclease resistant and can be used in the treatment of animals, including humans, having a bacterial infection. The treatment comprises administration of such nuclease resistant oligonucleotides, targeted to a nucleic acid or protein of the bacterium, and formulated with a carrier. A compound comprising this nuclease resistant oligonucleotide can be covalently linked to an antibiotic. The method is used to treat infections by a wide variety of Gram-positive and Gram-negative, or acid-fast, bacteria, in human and veterinary medicine. The methods are particularly used in immuno-compromised individuals (e.g. The methods are particularly used in immuno-compromised individuals (e.g. Cram-positive with acquired immunodeficiency syndrome or those receiving chemotherapy or radiation therapy), optionally in combination with, or fused to, antiviral or other antimicrobial oligonucleotides. Apart from theraptory cultures, foods, beverages and industrial processes The coligonucleotides are specific for bacteria, without affecting metabolism in mammalian cells. They may also activate RNase H and have a general, non-specific immune-stimulating effect. The oligonucleotides can be administered orally, intranasally, rectally, topically or by injection, optionally coupled to an agent (e.g. carbohydrate or polyamine) that
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Pred. No. 1e+03;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 18 BP; 9 A; 0 C; 0 G; 9 T; 0 U; 0 Other;
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Best Local Similarity 94.4%;
Matches 17; Conservative
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ID AAV21967 standard; DNA; 18
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Gaps

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2342

2325 GIGIGIGIGCGIGIGIG 1 GTGTGTGTGAGTGTGTGT

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Best Loca Matches

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This antisense oligonuclectide is nuclease resistant and can be used in the treatment of animals, including humans, having a bacterial infection. The treatment comprises administration of such nuclease resistant comprises administration of such nuclease resistant.

The treatment comprises administration of such nuclease resistant oligonuclectides, targeted to a nucleic acid or protein of the bacterium, and formulated with a carrier. A compound comprising this nuclease resistant oligonuclectide can be covalently linked to an antibiotic. The methods are particularly used in immuno-compromised individuals (e.g. parients with acquired immunodeficiency syndrome or those receiving chemotherapy or radiation therapy), optionally in combination with, or tuesed to, antiviral or other antimicrobial oligonuclectides. Apart from the oligonucleotides can be used to control bacteria in laboratory cultures, foods, beverages and industrial processes. The oligonucleotides are specific for bacteria, without affecting metabolism in mammalian calls. They may also activate Rnase H and have a general, in mammalian calls. They may also activate Rnase H and have a general, in mammalian calls. They may also activate Rnase H and have a general, one-specific immune-stimulating effect. The oligonucleotides can be administered orally, intransabally, rectally, topically or by injection, or prionally coupled to an agent (e.g. carbohydrate or polyamine) that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Treating bacterial infections in humans or animals with oligo:nucleotide(s) - resistant to nuclease and targetted to bacterial nucleic acid or proteins, also conjugates of these oligo:nucleotide(s) with antibiotics.
                                                                      Nuclease resistant antisense oligo NBT 140 targeted against (AT)9.
                                                                                                            Nuclease resistant; bacterial infection; antibiotic; target; veterinary medicine; treatment; human; industrial process; bacterial control; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 18 BP; 9 A; 0 C; 0 G; 9 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                 (OLIG-) OLIGOS ETC & OLIGOS THERAPEUTICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 49; Page 87; 163pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                        Thompson TL;
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                                     14-JUL-1998 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            enhances cellular uptake
                                                                                                                                                                                                                                                                                                                                                                                                                                        Arrow A, Dale RMK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1998-120687/11
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                      33-JUL-1997;
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                                                                                                                                                                                                                                                                                29-JAN-1998
                                                                                                                                                                                                 Synthetic.
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AAV21967,
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셤
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A method has been developed for labelling an oligonuclectide having a repeated sequence of (XY)n (where X and Y consists of a combination of adenine and thymine or uracil or guanine and cytosine, and n is an integer of 1 or more ) at the 3'-terminal side in which the repeated sequence is added and extended using a labelled body of the nucleotide constituting the repeated sequence and a DNA polymerase lacked in 5' to 3' exonuclease activity. The method can be used for detecting a generated and extended using a sensitivity up to ten times higher than prior art methods. The present sequence represents a primer used in an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                               Primer; oligonucleotide; labelling; detection; self-priming; PCR; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Labelling of an oligonucleotide - useful for detecting genes
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 18 BP; 9 A; 0 C; 0 G; 9 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                               (KAGA ) ZH KAGAKU & KESSEI RYOHO KENKYUSHO
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Primer SEQ ID NO:1 from JP11075880.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      example from the present invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 1; Page 7; 10pp; Japanese
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nes 17; Conserv
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Matches
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This invention describes a novel method for quantitating genetic instability independent of microsatellite alterations by treating a comparison genomic DNA from tumour cells and genomic DNA from tumour cells and genomic DNA from normal cells. The method involves the cells from the same individual with oligonucleotide primers selected from (i) a nucleotide sequence (CG)xRG, where R is a purine selected from adenine and guanine and x = 3-7, (ii) a nucleotide sequence (CG)xRK, where R is as in (i) and x = 3-7, (ii) a nucleotide sequence (CG)xRY, where R is as in (i) and x = 3-7, (ii) a nucleotide sequence (CG)xRY, where R is as in (i) and x = 3-7, (ii) a nucleotide sequence (CG)xRY, where R is a pyrimidine selected from cytosine, thymine, and uracil and x = 3-7, (iv) a nucleotide sequence (CA)xRY, where R is a purine selected from adenine and guanine and Y is a pyrimidine selected from cytosine, thymine, and uracil, and x = 6-16, (vii) a nucleotide sequence (CA)xRR, where R is a purine selected from adenine and guanine and X = 6-16, (vii) a nucleotide sequence (CA)xRR, where R is a purine selected from adenine and suracil, and x = 6-16, (vii) a nucleotide sequence (CA)xRR, where R is a purine selected from cytosine, thymine, and uracil, and x = 6-16, (vii) a nucleotide sequence (CA)xRR, where R is a purine selected from cytosine, thymine, and uracil.
                      A method has been developed for labelling an oligonucleotide having a repeated sequence of (XY)n (where X and Y consists of a combination of adenine and typosine, and n is an integer of 1 or more ) at the 3-terminal side in which the repeated sequence is added and extended using a labelled body of the nucleotide constituting the repeated sequence and a DNA polymerase lacked in 5 to 3' exonuclease activity. The method can be used for detecting a gene. The method can detect a gene in a sensitivity up to ten times higher than prior art methods. The present sequence represents a primer used in an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0.4%; Score 16.4; DB 1; Length 18; 94.4%; Pred. No. 1e+03; Ive 0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                        example from the present invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    94.48;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Anderson G, Stoler D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
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AAX77464/C
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This invention describes a novel method for quantitating genetic instability independent of microsatellite alterations by treating a comparising genomic DNA from through energy and genomic DNA from through and genomic DNA from through and genomic DNA from normal cells. The method involves the cells from the same individual comparison pair comprising genomic DNA from through and genomic DNA (G)xRG, where R is as in (1) and Y is a pyrimidine selected from cytosine, thymine, and uracil and x = 3-7, (iii) a nucleotide sequence (CG)xRY, where R is as in (1) and Y is a nucleotide sequence (CG)xRY, where R is as in (1) and x = 3-7, (iv) a nucleotide sequence (CG)xRY, where R is a pyrimidine selected from cytosine, thymine, and uracil and x = 3-7, (v) a nucleotide sequence (CG)xRY, where R is a purine selected from admine and Y is a pyrimidine selected from denine and guanine and Y is a pyrimidine selected from cytosine, thymine, and uracil, and x = 6-16, (vii) a nucleotide sequence (CA)xRY, where R is a pyrimidine selected from cytosine, where R is a purine selected from admine and x = 6-16, (vii) a nucleotide sequence (CA)xRY, where Y is a pyrimidine selected from cytosine, thymine, and uracil, and x = 6-16, (vii) a nucleotide sequence (CA)xRY, where Y is a pyrimidine selected from of the primers. The method is useful from deriving senociated with the various stages of neoplastic transformation and carcinogenesis. The method is rapid and simple
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from cytosine, thymine, and uracil and x = 6-16, and (ix) a combination of the primers. The method is useful for detecting genomic instability which are commonly associated with the various stages of neoplastic transformation and carcinogenesis. The method is rapid and simple
                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Primer; quantitation; genetic instability; tumour cell; detection; neoplastic transformation; carcinogenesis; ss.
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                                                                                                                                     0.4%; Score 16.4; DB 1; Length 18; 94.4%; Pred. No. 1e+03; ve 0; Mismatches 1; Indels
                                                                                                  Sequence 18 BP; 10 A; 8 C; 0 G; 0 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Quantitating genetic instability.
                                                                                                                                                                                                                       2316 TCTGTGTGTGTGTGTG 2333
                                                                                                                                                                                                                                                                                                                                                                BP.
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                                                                                                                                                          Local Similarity 94.4%;
les 17; Conservative
                                                                                                                                                                                                                                                              18 TTTGTGTGTGTGTGTGTG
                                                                                                                                                                                                                                                                                                                                                              AAX77457 standard; DNA; 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US5912147 primer 1.
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                                                                                                                                         Query Match
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Matches
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8X33333
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The present invention relates to methods for treating or preventing cancer, involving administering to a subject having or at risk of developing cancer immunostimulatory nucleic acids that induce expression of cell surface antigens and antibodies. The methods are useful for treating or preventing cancer such as basal cell carcinoma, bladder cancer, bone cancer, brain and central nervous system (CNS) cancer, breast cancer, cervical cancer, coln and rectum cancer, connective tissue cancer, oesophagaal cancer, elective cancer, Hodgkin's lymphoma, melanoma, myeloma, oral cavity cancer, overian cancer, prostate cancer, rhabdomyosarcoma, skin cancer, stomach cancer, besticular cancer, rhabdomyosarcoma, skin cancer, stomach cancer, besticular cancer, and uterine cancer. The present sequence is an immunostimulatory oligonucleotide described in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Treating or preventing cancer, such as basal cell carcinoma, comprises administering immunostimulatory nucleic acids that induce expression of cell surface antigens and antibodies to a subject having or at risk of
                                                             Antibody-induced cell lysis; cancer; immunostimulatory; CD20; angiogenesis; metastasis; cytostatic; phosphorothioate backbone; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Antibody-induced cell lysis; cancer; immunostimulatory; CD20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 16.4; DB 1; Length 18;
Pred. No. 1e+03;
0; Mismatches 1; Indels
                                                                                                                                                                                                      'note= "phosphorothioate backbone"
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                             Immunostimulatory nucleic acid SEQ ID NO: 85.
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                                                                                                                                         Location/Qualifiers
                                                                                                                                                        1, .18
/*tag= a
/mod_base= OTHER
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(first entry)
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Best Local Similarity 94.4
Matches 17; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              developing cancer.
                                                                                                                                                                                                                                       WO200197843-A2
                                                                                                                                                           modified base
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 16-APR-2002
                                                                                                                                                                                                                                                                        27-DEC-2001.
                                                                                                             Synthetic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention relates to Simple Sequence Repeats (SSRs) from clover species. SSRs, also called microsatellites, are based on a 1-7 nucleotide core element which is tandemly repeated. The SSR array is embedded in complex flanking DNR. SSRs are ideal markers for genome mapping, trait mapping and marker-assisted selection. The SSRs may be used in methods for selecting genes in clover/legume breeding. The SSRs are also useful for DNA profiling of clover varieties and for testing the purity of legume seed batches. The present sequence is a SSR motif, which
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel simple sequence repeats in clover species useful for selection of genes in legume breeding, for profiling legume species varieties and for testing the purity of legume seed batches.
                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                    Simple Sequence Repeat; SSR; clover; microsatellite; genome mapping; trait mapping; marker-assisted selection; gene selection; legume; DNA profiling; breeding; ds.
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 Score 16.4; DB 1; Length 18;
Pred. No. 1e+03;
                               1; Indels
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                                 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (AGRI-) AGRIC VICTORIA SERVICES PTY LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     was used in the present invention
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                                                                2334 CGTGTGTGTGTGTGTG 2351
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                                                                                                                                                                             BP.
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28-MAR-2000; 2000AU-00006520.
   0.4%;
                                                                                    2328 TGTGTGCGTGTGTGTG
                  94.48;
                                                                                                                                                                             AAI64450 standard; DNA; 18
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                                 17; Conservative
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Matches 17; Conser
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                                                                                                                                                                                                             AAI64450;
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    Query Match
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ABL38718
ID ABL387:
XX
AC ABL387:
XX
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Gaps

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Best Loc Matches

Fondon JW;

Minna JD,

(TEXA) UNIV TEXAS SYSTEM. Garner HR, Wren JD,

99US-00475947. 99US-00475947.

31-DEC-1999; 31-DEC-1999;

29-OCT-2002

Homo sapiens. US6472154-B1.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cancer, leukaemia, liver cancer, lung cancer, Hodgkin's lymphoma, non-Hodgkin's lymphoma, melanoma, myeloma, oral cavity cancer, ovarian cancer, pancreatic cancer, prostate cancer, rhabdomyosarcoma, skin cancer, stommach cancer, testicular cancer, and uterine cancer. The present sequence is an immunostimulatory oligonucleotide described in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention relates to methods for treating or preventing cancer, involving administering to a subject having or at risk of developing cancer immunostimulatory nucleic acids that induce expression of cell surface antigens and antibodies. The methods are useful for treating or preventing cancer such as basal cell carcinoma, bladder cancer, bone cancer, brain and central nervous system (CNS) cancer, breast cancer, cervical cancer, colon and rectum cancer, connective tissue cancer, oesophageal cancer, eye cancer, kidney cancer, larymx cancer, leukaemia, liver cancer, lung cancer, Hodgkin's lymphoma, non-
                                                                                                                                                                                                                                                                                                                                                                                                                                      Treating or preventing cancer, such as basal cell carcinoma, comprises administering immunostimulatory nucleic acids that induce expression of cell surface antigens and antibodies to a subject having or at risk of developing cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EST; expressed sequence tag; ss; polymorphic repeat; tandem repeat; polymorphic marker prediction of ubiquitous simple sequences; POMPOUS; Rep-X; human; genetic disease; drug-treatment; Machado-Joseph; Haw River syndrome; Huntington's disease; fragile-X syndrome; Predreich's ataxis; myotonic dystrophy; hyperandrogenaemia; spinal atrophy; bulbar atrophy; spinocerebellar ataxia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
angiogenesis; metastasis; cytostatic; phosphorothioate backbone; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0.4%; Score 16.4; DB 1; Length 18;
4.4%; Pred. No. 1e+03;
ve 0; Mismatches 1; Indels
                                                                                                                                            /note= "phosphorothioate backbone"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 18 BP; 9 A; 0 C; 0 G; 9 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EST polymorphic DNA repeat polynucleotide #104.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Page 116; 312pp; English.
                                                                    Location/Qualifiers
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                                                                                                          J= a
base= OTHER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              exemplification of the invention
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                                                                                                                                                                                                                                                       22-JUN-2001; 2001WO-US020154.
                                                                                                                                                                                                                                                                                           22-JUN-2000; 2000US-0213346P
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Best Local Similarity 94.4%;
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                                                                                                          tag=
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                                                                                                                                                                                  WO200197843-A2
                                                                      Key
modified_base
                                                                                                                                                                                                                   27-DEC-2001
                                  Synthetic
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comprises detecting tangence to twenthing a dataset comprises detecting tandem repeats in a target coding sequence, scoring the repeats for polymorphic probability and generating a dataset correlating the repeats with polymorphic probability to identify a correlating the repeats with polymorphic probability to identify a candidate polymorphic repeat. The computational methods (polymorphic marker prediction of ubiquitous simple sequences, POMPOUS, and Rep-X) are useful for identifying and detecting candidate polymorphic repeats in useful for identifying and detecting candidate polymorphic repeats in the use of the seases, predispositions or adverse drug-treatment reactions. Examples of diseases linked to nucleotide repeats are Machado-Joseph, Haw River syntome, Huntingron's disease, fragile-X syndrome, Predistorby, hyperandrogenaemia, spinal and bulbar atrophy and spinocerebellar ataxia. The sequences presented in ABX79676-ABX80022 are the polymorphic repeats identified for a search of human ESTs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention discloses a method for identifying a candidate polymorphic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 human; T-cell associated disease; Wheta; autoimmune disease; degenerative nervous system disease; graft versus host disease; hypersensitivity disease; infectious disease; neoplastic disease; dadison a disease; attenties; dadison system disease; multiple sclerosis; Alzhelmer's disease; hypersensitivity disease; type I hypersensitivity; Goodpasture's syndrome; type IV hypersensitivity; Goodpasture's syndrome; type IV hypersensitivity; leprosy; infectious disease; viral infection; HIV; fungal infection; Candida; parasitic infection; schistosome; filaria; bacterial infection; Mycobacterium; neoplastic disease; lymphoproliferative disease; leukaemia; lymphopma; cancer; brain cancer;
                                                                                                                                                                                                                                                                                                                                                                   tandem
                                                                                                                                                                                                                                                                                                                                          Identifying a candidate polymorphic repeat within a coding sequence, understanding or treating genetic disease, comprises detecting tandem repeats in a target coding sequence and scoring the repeats for polymorphic probability.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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44.4%; Pred. No. 1e+03;
ve 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 18 BP; 8 A; 0 C; 1 G; 9 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human Vbeta gene repeat sequence #432.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example; Col 385; 588pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2822 GTATATATACATATAT 2839
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les 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GTATATATATATATAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                   WPI; 2003-208818/20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              breast cancer; ds
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Matches
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17-OCT-2002

Vbeta gene

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The present invention describes a method for detecting the presence of polymorphisms associated with inflammatory bowel diseases such as ulcerative colitis and Crohn's disease. The methods can be used to detect the presence of genetic polymorphisms associated with inflammatory bowel disease and correlating their occurrence with disease astates. They may be used in this way for phenotypic correlations, forensics, paternity testing, medicine and genetic analysis. The present sequence is a polymorphic site described in the exemplification of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Testing for the presence of polymorphisms associated with inflammatory bowel disease, using a hybridization assay.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 short interfering nucleic acid; siNA; downregulation; inhibition; mitogen-activated protein kinase; MAP kinase; MAPK; RNA interference; cytostatic; anorectic; antidiabetic; antiinflammatory; antiasthmatic; immunosuppressive; antibacterial; antirheumatic; antiarthritic; antipsoriatic; gastrointestinal; obesity; diabetes; tumour; inflammatory disease; asthma; septic shock; rheumatoid arthritis; psoriasis; inflammatory bowel disease; drug screening; esentic engineering; pharmacogenomic; gene mapping; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mitogen activated protein kinase siNA oligonucleotide SEQ ID NO:522.
                                                            /*tag= a
/note= "SNP, optionally T or C at this position"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0.4%; Score 16.4; DB 1; Length 19;
89.5%; Pred. No. 1.1e+03;
tive 0; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                         WHED ) WHITEHEAD INST BIOMEDICAL RES
                                                                                                                                                                                                                                                                                                                                                            (ELLI-) ELLIPSIS BIOTHERAPEUTICS CORP
              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; Page 80; 463pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               255 CAAGAAGCTGCTGGCCGTG 273
                                                                                                                                                                                                                                                                                                                                                                                                            Lander ES,
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                                                                                                                                                                                                                                                                        99US-0170257P.
                                                                                                                                                                                                                          11-DEC-2000; 2000WO-US033632.
                                                                                                                                                                                                                                                                                           10-APR-2000; 2000US-0196046P
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2001-367874/38.
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                                                                                                                                    WO200142511-A2
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                                      misc_feature
                                                                                                                                                                                                                                                                        10-DEC-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to a kit for diagnosing and treating T-cell associated diseases which comprises a panel of nucleic acid primers specifically priming and allowing amplification of each Vbetage gene, VbetaRNA or CDNA. The kit is useful for diagnosing organ transplant rejection and diagnosing and treating T-cell associated diseases include autoimmune diseases, degenerative nervous system diseases.

Coraft versus host disease. Autoimmune diseases include Addison's disease, atrophic gastritis. Degenerative nervous system diseases, infectious disease, atrophic gastritis Degenerative nervous system diseases include multiple of clerosis and Alzheimer's disease. Hypersensitivity diseases include Type I hypersensitivities such as those present in Coodpasture's syndrome and Type IV hypersensitivities such as those force and the veast genue Candida, parasitic infections such as those caused by chistosomes, filaria and bacterial infections such as those caused by schistosomes, filaria and bacterial infections such as those caused by Mycobacterium. Neoplastic diseases include lymphoprofiferative diseases
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Kit for diagnozing and treating T-cell associated diseases e.g. autoimmune, degenerative nervous system and infectious disease, comprises nucleic acid primers specifically priming and allowing amplification of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; inflammatory bowel disease; Crohn's disease; ulcerative colitis; single nuclectide polymorphism; SNP; chromosome 19p13; paternity test; chromosome 5q31-33; forensic test; gene therapy; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      such as cancer of the brain,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  such as leukaemias, lymphomas and cancers such as cancer of the brain
breast. The present sequence represents a Vbeta gene repeat sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human inflammatory bowel disease associated polymorphic site #991.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 19 BP; 10 A; 0 C; 0 G; 9 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; SEQ ID NO 836; 164pp; English.
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                                                                                                                                                                                                            94US-00309335
95US-00531241
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Best Local Similarity 94.4's
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В
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                                                                        US2002150891-A1
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19-SEP-1995;
                                                                                                                                                                                                                                                                               (HOOD/) HOOD
(ROWE/) ROWEN
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                               Homo sapiens
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Gaps

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28-JAN-2003; 2003WO-US002510.

Homo sapiens

AAH91916;

AAH91916/c
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AC AAH91
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DT 09-0C
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MW Humar
XW Humar
XW Sing:
XX
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Humar

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Siminovitch

Rioux J,

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WO2003072590-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           that downregulates expression of a mitogen-activated protein kinase (MAPK) genes by RNA interference. Also described: (1) a method for modulating expression of MAPK genes in cells, tissue explants or organisms by introduction of MAPK genes in cells, tissue explants or organisms by introduction of SINA; (2) kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or complexes of siNA; and (4) ectors that express siNA and cells containing these vectors. MAPK siNAs have cytostatic, anorectic, antidabetic, antiminamatory.

The antiathmatic, immunosuppressive, antibacterial, antirheumatic, antisposiatic and gastrointestinal activities. The MAPK siNAs can be used to modulate the expression of MAPK genes, in cells, tissue explants or organisms, e.g. for treating obesity; diabetes types I can in a wide range of tumours, and inflammatory diseases asthma, septic shock, rheumatoid arthritis, psoriasis and inflammatory bowel disease. They can also be used for drug screening; pharmacogenomics; studying gene function and gene mapping (e.g. of single-nucleotide polymorphisms). The present sequence represents a MAPK sinA which is used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              present invention describes a short interfering nucleic acid (siNA)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             short interfering nucleic acid, useful e.g. for treatment and mosis of cancer, downregulates expression of mitogen-activated
                                                                                                                                                                                                                                                                                                                                                                                                                                     Chowrira B;
                                                                                                                                                                                                                                                                                                                                                                                                                                     Usman N, Haeberli P,
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                                                                                                                                                                                                                                                                                                                                                        SIRN-) SIRNA THERAPEUTICS INC.
                                                                         2002US-0363124P.
2002US-0386782P.
2002US-0406784P.
                                                                                                                                                                                            2002US-0408378P.
                                                                                                                                                                                                                                     2002US-0409293P
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                                    2002US-0358580P
                                                                                                                                                                                                                                                                                                                                                                                                                                     Mcswiggen J, Beigelman L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           protein kinase genes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  diagnosis of cancer,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2003-689980/65.
                                                                     11-MAR-2002;
06-JUN-2002;
29-AUG-2002;
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                                                                                                                                      Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       short interfering nucleic acid; siNA; downregulation; inhibition; mitogen-activated protein kinase; MAP kinase; MAPK; RNA interference; cytostatic; anorectic; anticibatic; anticilalmamatory; antiasthmatic; immunosuppressive; antibacterial; antirheumatic; antiarchritic; antipsoriatic; gastrointestinal; obesity; diabetes; tumour; inflammatory disease; asthma; septic shock; rheumatord arthritis; psoriasis; inflammatory bowel disease; drug screening; genetic engineering; pharmacogenomic; gene mapping; ss.
                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mitogen activated protein kinase sina oligonucleotide SEO ID NO:417.
                                                         ö
0.4%; Score 16.4; DB 1; Length 19; 33.3%; Pred. No. 1.1e+03; ve 2; Mismatches 1; Indels
                                                                                                              2905 GGCAGGCATGGCCCTGGG 2922
                                                                                                                                      BP
                              83.3%;
                                                                                                                                                                                                                                                                                                   ADE29795 standard; RNA; 19
                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                              Local Similarity 83.3
Les 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                         29-JAN-2004
                                                                                                                                                                                                                                                                                                                                                     ADE29795;
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셤 ઠે

Synthetic

RESULT 877
ADE29795/C
XX
XX
AC ADE297
XX
DT 29-JAN
XX
XX
DD Mitoge
XX
KW short
KW mitoge
KW mito

```
that downregulates expression of a mitogen-activated protein kinase that downregulates expression of a mitogen-activated protein kinase (MAPK) genes by RNA interference. Also described: (1) a method for modulating expression of MAPK genes in cells, tissue explants or corganisms by introduction of siNA; (2) kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or complexes of siNA; and (4) vectors that express siNA and cells containing these vectors. MAPK siNAs aver cytostatic, anoractic, antibacterial, antihalammatory, antiathmatic, antipsoriatic and gastrointestinal activities. The MAPK antistrict, antipsoriatic and gastrointestinal activities. The MAPK antister explants or organisms, e.g. for treating obesity; diabetes types in sinks can be used to modulate the expression of MAPK genes, in cells, tissue explants or organisms, e.g. for treating obesity; diabetes types and il; a wide range of tumours, and inflammatory diseases (asthma, espetic shock, rheumatoid arthritis, psoriasis and inflammatory bowel disease). They can also be used for drug screening; pharmacogenomics; cidentification, mand validation; genetic engineering; pharmacogenomics;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      double-stranded short interfering nucleic acid; short interfering nucleic acid; siNA; downregulation; vascular endothelial growth factor receptor; VEGFR; antiangiogenic; cytostatic; antidiabetic; ophthalmological; antiathritic; antipsoriatic; nephrotropic; gynaecological; angiogenesis-associated condition; cancer; diabetic retinopathy; macular degeneration; neovascular glaucoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sequence represents a MAPK sinA which is used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention describes a short interfering nucleic acid (siNA)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                    New short interfering nucleic acid, useful e.g. for treatment and diagnosis of cancer, downregulates expression of mitogen-activated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          le-nucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human VEGFR1 short interfering nucleic acid (siNA) SEQ ID NO:390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                  Chowrira B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 16.4; DB 1; Length 19;
Pred. No. 1.1e+03;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       studying gene function and gene mapping (e.g. of sing)
                                                                                                                                                                                                                                                                                                                                                Usman N, Haeberli P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 19 BP; 3 A; 8 C; 5 G; 0 T; 3 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 3; SEQ ID NO 417; 164pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2905 GGCAGGCATGGCCTGGG 2922
                                                                                                                                                                                                                                                                                                       (SIRN-) SIRNA THERAPEUTICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADF36101 standard; RNA; 19 BP.
                                                                                                                                                                                         29-AUG-2002; 2002US-0406784P.
05-SEP-2002; 2002US-0408378P.
09-SEP-2002; 2002US-0409293P.
15-JAN-2003; 2003US-0440129P.
                                                                                                                                                2002US-0363124P
2002US-0386782P
                                                                                   28-JAN-2003; 2003WO-US002510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19 GGCAGGCATGGCCCTGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            94.48;
                                                                                                                                                                                                                                                                                                                                                  Mcswiggen J, Beigelman L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12-FEB-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 94.4
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein kinase genes.
                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2003-689980/65.
                                                                                                                                                  11-MAR-2002;
06-JUN-2002;
                                          04-SEP-2003
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double-stranded short interfering nucleic acid; short interfering nucleic acid; siNh; downregulation; saket interfering nucleic acid; siNh; downregulation; vascular endothelial growth factor receptor; VEGFR; antiangiogenic; cytostatic; antidiabetic; ophthalmological; antiarthritic; antipsoxiatic; nephrotropic; gynaecological; angiogenesis-associated condition; cancer; diabetic retinopathy; macular degeneration; neovascular glaucoma; arthritis; psoriasis; endometriosis; angiofibroma;

Human VEGFR1 short interfering nucleic acid (siNA) SEQ ID NO:817

(first entry)

12-FEB-2004

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The present invention describes a double-stranded short interfering nucleic acid (siNA) that downregulates expression of the vascular endothelial growth factor receptor (WEGFR) gene. Also described: (1) a siNA that downregulates the VEGF gene; (2) kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or complexes of siNA; (4) vectors that express siNA; and (5) single-stranded siNA with similar properties. The siNAs have antiangiogenic, cytostatic, antidiabetic, or poptrates. The siNAs are potentially gynaecological activities. The siNA are useful for modulating (downregulating) the expression of VEGFR genes. The siNA are potentially useful for treating a wide range of angiogenesis—associated conditions, particularly cancers, diabetic retinopathy, macular degeneration, neovascular glaucoma, arthritis, psoriasis, endometriosis, angiofibroma, and polycystic kidney disease. The siNA may also be useful for diagnosis, drug screening, studying gene function, and also for gene mapping (e.g. of single-mucleotide polymorphisms). The present sequence is used in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New double-stranded interfering nucleic acid, useful e.g. for treatment and diagnosis of cancer, downregulates the vascular endothelial growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0.4%; Score 16.4; DB 1; Length 19; 50.0%; Pred. No. 1.1e+03; Ive 8; Mismatches 1; Indels
arthritis; psoriasis; endometriosis; angiofibroma;
polycystic kidney disease; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Seguence 19 BP; 0 A; 0 C; 11 G; 0 T; 8 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 3; SEQ ID NO 390; 207pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pavco P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2322 TGTGTGTGTGTGTGTG 2339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18
                                                                                                                                                                                                                                                           06-JUN-2002; 2002US-0386782P.
03-JUL-2002; 2002US-0393796P.
29-JUL-2002; 2002US-0399348P.
29-AUG-2002; 2002US-0406784P.
                                                                                                                                                                                                                                                                                                                               05-SEP-2002; 2002US-0408378P.
09-SEP-2002; 2002US-0409293P.
04-NOV-2002; 2002US-00287949.
                                                                                                                                                                                                           2002US-0358580P.
2002US-0363124P.
2002WO-US017674.
                                                                                                                                                                          2003WO-US005022
                                                                                                                                                                                                                                                                                                                                                                                  27-NOV-2002; 2002US-00306747
15-JAN-2003; 2003US-0440129P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mcswiggen J, Beigelman L,
                                                                                                                                                                                                                                                                                                                                                                                                                                      (RIBO-) RIBOZYME PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             factor receptor gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2003-679876/64.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                      WO2003070910-A2.
                                                                                                                                                                                                                         11-MAR-2002;
29-MAY-2002;
                                                                      Homo sapiens
                                                                                                                                                                          20-FEB-2003;
                                                                                                                                      28-AUG-2003
                                                    Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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Matches
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2002US-0386782P. 2002US-0393796P. 2002US-0399348P.

06-JUN-2002; 03-JUL-2002;

29-JUL-2002; 29-AUG-2002;

2002US-0363124P. 2002WO-US017674

2003WO-US005022

20-FEB-2003;

28-AUG-2003

20-FEB-2002; 11-MAR-2002; 29-MAY-2002;

WO2003070910-A2 Homo sapiens.

Synthetic.

2002US-0409293P.

2002US-00306747

27-NOV-2002;

04-NOV-2002;

15-JAN-2003; 2003US-0440129P

(RIBO-) RIBOZYME PHARM INC

2002US-0406784P

05-SEP-2002;

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The present invention describes a double-stranded short interfering nucleic acid (siNA) that downregulates expression of the vascular endothelial growth factor receptor (VEGFR) gene. Also described: (1) a cin that downregulates the VEGF gene; (2) kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or complexes of siNA; (4) vectors that express siNA; and (5) single-stranded siNA with similar properties. The siNAs have antianajogenic, cytostatic, nephrotropic and gynaecological activities. The siNA are useful for modulating commanded single the expression of VEGFR genes. The siNA are potentially downregulating) the expression of VEGFR genes. The siNA are potentially cureful for treating a wide range of angiogenessis-associated conditions, particularly cancers, diabetic relinopathy, macular degeneration, particularly cancers, diabetic relinopathy, macular degeneration, consumptivity dispersive vident dispersive single dentification and validation, genetic engineering, studying gene function, and also for gene mapping (e.g. of single-incleant sequence is used in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New double-stranded interfering nucleic acid, useful e.g. for treatment and diagnosis of cancer, downregulates the vascular endothelial growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 16.4; DB 1; Length 19;
Pred. No. 1.1e+03;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 19 BP; 8 A; 11 C; 0 G; 0 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 3; SEQ ID NO 817; 207pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pavco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 94.4%;
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mcswiggen J, Beigelman L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           factor receptor gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2003-679876/64.
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2322 TGTGTGTGTGCGTGTG 2339

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ADF36528 standard; RNA; 19

RESULT 879

ADF36528 ADF36528/C ID ADF365 XX AC ADF365 XX ss; siNA; human; BCL2; short interfering nucleic acid; RNA interference; cytostatic; immunosuppressive; virucide; anti-HIV; cancer; autoimmune disease; viral infection; HIV.

Human BCL2 siNA lower sequence SEQ ID NO:104

(first entry)

12-FEB-2004

ADF49376;

ADF49376 standard; RNA; 19 BP

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88; 81NA; human; BCL2; short interfering nucleic acid; RNA interference; cytostatic; immunosuppressive; virucide; anti-HIV; cancer; autoimmune disease; viral infection; HIV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to a novel short interfering nucleic acid (siNA) that downregulates expression of the BCL2 gene by RNA interference. A siNA of the invention has cytostatic, immunosuppressive, virucide, and anti-HFV activity. The siNA are useful for modulation (inhibition) of expression or activity of BCL2 by RNA interference. siNA are used to modulate expression of BCL2 genes, in cells, tissue explants or organisms, e.g. for treating cancer, autoimmune diseases and viral infections (including by HIV) but also for drug screening, diagnosis, target identification and validation, genetic engineering, pharmacogenomics, studying gene function and gene mapping (e.g. of sing represent siNA of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New short interfering nucleic acid, useful e.g. for treatment and diagnosis of cancer or autoimmune disease, downregulates expression of the BCL2 gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0.4%; Score 16.4; DB 1; Length 19; 94.4%; Pred. No. 1.1e+03; ve 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 19 BP; 4 A; 9 C; 3 G; 0 T; 3 U; 0 Other;
                                                                                                                                                                                                  Human BCL2 siNA lower sequence SEQ ID NO:518.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 3; SEQ ID NO 518; 148pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                   20-FEB-2002; 2002US-0358580P.
11-MAR-2002; 2002US-0363124P.
06-UUN-2002; 2002US-0386782P.
18-UUL-2002; 2002US-0396905P.
29-AUG-2002; 2002US-0406784P.
05-SEP-2002; 2002US-0406784P.
                                                                                                   ADF49790 standard; RNA; 19 BP
                                                                                                                                                                                                                                                                                                                                                                                                     18-FEB-2003; 2003WO-US004908
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      L5-JAN-2003; 2003US-0440129P
(RIBO-) RIBOZYME PHARM INC.
                                                                                                                                                                    12-FEB-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mcswiggen J, Beigelman L;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ouery Match
Best Local Similarity 94.4*
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2003-712622/67.
                                                                                                                                                                                                                                                                                                                                    WO2003070969-A2.
                                                                                                                                                                                                                                                                                                       Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                     28-AUG-2003
                                                                                                                                    ADF49790;
                                                                                    ADF49790,
                    셤
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New short interfering nucleic acid, useful e.g. for treatment and diagnosis of cancer or autoimmune disease, downregulates expression of the BCL2 gene.

11-MAR-2002; 2002US-0363124P. 06-UTV-2002; 2002US-03867B2P. 18-UTL-2002; 2002US-0396905P. 29-AUG-2002; 2002US-0406784P. 05-SEP-2002; 2002US-0408378P. 15-JAN-2003; 2003US-0440229P.

(RIBO-) RIBOZYME PHARM INC Mcswiggen J, Beigelman L;

MPI; 2003-712622/67.

18-FEB-2003; 2003WO-US004908

20-FEB-2002;

WO2003070969-A2 Homo sapiens.

28-AUG-2003

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The invention relates to a novel short interfering nucleic acid (siNA) that downregulates expression of the BCL2 gene by RNA interference. A sulf A feet invention has cytostatic, immunosupressive, virucide, and anti-HIV activity. The SINA are useful for modulate succession or activity of BCL2 by RNA interference. SiNA are used to expression or activity of BCL2 by RNA interference. SiNA are used to organisms, e.g. for treating cancer, autoimmune diseases and viral infections (including by HIV) but also for drug screening, diagnosis, traget infentification and validation, general expineering, pharmacogenomics, studying gene function and gene mapping (e.g. of single-nucleotide polymorphisms). The sequences shown in ADF49273-ADF50143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0.4%; Score 16.4; DB 1; Length 19; 72.2%; Pred. No. 1.18+03; tive 4; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 19 BP; 3 A; 3 C; 9 G; 0 T; 4 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 3; SEQ ID NO 104; 148pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1873 GTGGAGGAGCTCTTCAAG 1890
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           represent sina of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 GUGGAGGAGCUCUUCAGG 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAT41101 standard; DNA; 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    03-DEC-1996 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 72.2
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAT41101;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 882
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single

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Gaps

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1873 GTGGAGGAGCTCTTCAAG 1890

18

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RESULT 881

ADF49376

94.48;

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The present sequence is an exon 8 primer for the polymerase chain reaction-single stranded conformational polymorphism (PCR-SSCP) analysis of the endothelial nitrogen monoxide synthase (eNOS) gene. The PCR-SSCP analysis was used in an example of genetic screening method for diseases associated with coronary arterial spasm, which comprises determining if 1 or more specific nucleotides in the eNOS gene have been substituted, specifically G894T, C774T, T(-786)C, A(-922)G and T(-1468)A. Screening for diseases associated with coronary spasm, e.g angina pectoris, cannot be easily carried out by existing methods, this method allows rapid and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human nucleolin phosphorothioate antisense oligonucleotide, SEQ ID NO:42.
                                                                                                                                                                                                                                                                                                          Genetic screening for diseases associated with coronary arterial spasm by assessment of the occurrence of specific mutation(s) of the endothelial nitrogen monoxide synthase gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human nucleolin; P92; C23; phosphoprotein; ribosome biogenesis; ribosome transport; cytokinesis; nucleogenesis; cell proliferation; cell growth; transcriptional repression; replication; asignal transduction; chromatin decondensation; Ag-NOR family; nucleolin antibody; systemic connective tissue disease; SLE; systemic lupus erythematosus; celeroderma-like chronic graft versus host disease; scleroderma-like chronic graft versus host disease; expression inhibition; tumour formation; cancer; inflammation; immune disorder; phosphorothioate; antisense oligonucleotide; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 0.4%; Score 16.4; DB 1; Length 20; Best Local Similarity 94.4%; Pred. No. 1.1e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 20 BP; 6 A; 10 C; 2 G; 2 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                          Example 1; Page 14; 47pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3064 TGTTCCCACACCCCAACA 3081
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3 TGATCCCACACCCCAACA 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAC92592 standard; DNA; 20 BP
                                              96WO-JP003324.
                                                                                           95JP-00319504.
96JP-00168761.
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                                                                                                                                                                  SHIO ) SHIONOGI & CO LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (ISIS-) ISIS PHARM INC
                                                                                                                                                                                                              Yoshimura M;
                                                                                                                                                                                                                                                                WPI; 1997-289303/26.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          easy detection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
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                                                 13-NOV-1996;
                                                                                             13-NOV-1995;
                                                                                                                   28-JUN-1996;
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22-MAY-1997
                                                                                                                                                                                                                 Yasue H,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          primers T41001-T41382 are derived from novel human gene signature (GS) sequences which did not match with sequences deposited in Genbank release 76. The GS sequences (T19001-T26837) were obtained from 3 -directed cDNA libraries prepared from various human tissues; synchesis of CDNA was initiated from the 3 -end of mRNA by using poly(T) as the sole primer. Each library is constructed so as to reflect accurately the relative abundance of different mRNAs in the particular tissue from which it was derived. The appearance frequency of a given GS in a cDNA library can be determined (esp. using primers and probes derived from the GS sequences) as a means of disgnosing abnormal cell function or for recognising different cell types. The primers T41101-2 amplify clone pm2619 which comprises the GS HUMGS001562 (T20562), located on chromosome 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Single-stranded DNA for identifying gene signatures - isolated from 3'-directed human cDNA library that reflects relative abundance of corresp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Exon 8; PCR primer; single stranded conformational polymorphism; SSCP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                         Gene signature; messenger RNA; mRNA; relative abundance; frequency; human; cloning; mapping; non-biased library; diagnosis; detection; cell typing; abnormal cell function; primer; PCR; amplification; polymerase chain reaction; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Primer for exon 8 of endothelial nitrogen monoxide synthase gene
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genetic screening, coronary arterial spasm; angina pectoris; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 16.4; DB 1; Length 20; Pred. No. 1.1e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Indels
  gene signature HUMGS01562-derived sense primer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 20 BP; 6 A; 6 C; 4 G; 4 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 7; Fig 7; 2245pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1250 TCGGCATTGACAAGGACC 1267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      mRNA in specific human tissues.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Okubo K;
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                                                                                                                                                                                                                                                                                                                                                                                                       (MATS/) MATSUBARA K. (OKUB/) OKUBO K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1995-206931/27.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matsubara K,
                                                                                                                                                                                                                 WO9514772-A1.
                                                                                                                                                                                                                                                                                                            11-NOV-1994;
                                                                                                                                                                                                                                                                                                                                                           12-NOV-1993;
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                                                                                                                                                                     Synthetic.
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Best Loca Matches

RESULT 883

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Adrigation Adrigation

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Gaps

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1; Indels

Bennett CF, Cowsert LM;

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Sequences AAC92560-C92639 represent antisense oligonucleotides targetted to the human nucleolin gene, which inhibit its expression. The antisense oligonucleotides were designed to target different regions of the human nucleolin mRNA, and were analysed for their effect on nucleolin mRNA in the nucleolin mRNA is a levels by quantitative real-time PCR. Nucleolin (also known as P92 or C23) is the most abundant nucleolar phosphoprotein in actively growing cells. Nucleolin primarily participates in ribosome biogenesis and cells. Nucleolin primarily participates in ribosome biogenesis and cells. The nucleolar via a ribonucleoprotein consensus sequence. Thosomes in the nucleolus via a ribonucleoprotein consensus sequence. However, it has also been shown to be involved in cytokinesis, nucleogenesis, cell proliferation and growth, transcriptional repression, replication, signal transduction, and chromatin decondensation. Nucleolin is a member of the Ag-NOR (active ribosomal gene located in the nucleolar ciposes, and whose expression is associated with the prediction of tumour growth rate. The presence of antibodies against nucleolin are associated with systemic connective tissue diseases such as systemic lupus erythemacrosus (SLE) and selexodermalike chronic graft versus host disease. The oligonucleotides of the invention are useful for diagnosis, prevention and treatment of conditions associated with nucleolin
                                                                                                               Novel antisense compound targeted to human nucleolin which specifically hybridizes with and inhibits the expression of human nucleolin, useful for modulating the expression of nucleolin in cells.
                                                                                                                                                                                                                               Claim 14; Col 41-42; 41pp; English.
                                                      WPI; 2001-079848/09.
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expression, such as tumour formation, immune disorders and inflammation

Sequence 20 BP; 4 A; 7 C; 1 G; 8 T; 0 U; 0 Other;

Ouery Match 0.4%; Score 16.4; DB 1; Length 20; Best Local Similarity 94.4%; Pred. No. 1.1e+03; Matches 17; Conservative 0; Mismatches 1; Indels 1353 GGAGATGATGAAGATGAT 1370 19 GAAGATGATGAAGATGAT 2 ઠે ద

Gaps

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ABS97835 standard; DNA; 20 BP ABS97835; RESULT 885

Human NADPH quinone oxidoreductase 2 (NQO2) polymorphic sequence #43

23-DEC-2002 (first entry)

Human; ds; cytochrome P450 A1; CYP4501A1; UGT2B4; MDR1;

w diveneration receptor beta1; ADBR1; arth hydrocarbon; AHR; MRP3; NRI1;

adrenergic receptor beta1; ADBR1; arth hydrocarbon; AHR; MRP3; NRI12;

w arryl hydrocarbon receptor nuclear translocator; ARNT; cathepsin S; CTSS;

cyclooxgense 2; COX2; diazepam binding inhibitor; DB1; haematological;

w poxide hydroxylase 2; EPHX2; 5-lipoxygense activating protein; FLAP;

w plutathione-S-transferase 12; GST12; histamine-N-methyl transferase;

HNMT; kallikrein 2; KIK2; inicotinamide-N-methyl transferase;

w NADPH quinone oxidoreductase 23; NQO2; sulfotransferase; NNMT;

w UDP-glucuronosyl transferase 284; UDP-glucuronosyl transferase 287;

w UDP-glucuronosyl transferase; UGT2B15; urokinase receptor;

w ultidrug resistance associated protein 3; cancer; prostate;

multidrug resistance associated protein 3; cancer; prostate;

multidrug resistance associated protein 3; cancer; prostate;

altered drug metabolism; cardiovascular function; colorectal tumour;

central nervous system; plimonary; immunological; SNP;

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BP.

ACC49689 standard; DNA; 20

ACC49689/c ID ACC496 RESULT 886

Homo sapiens

single nucleotide polymorphism.

The invention relates to the Sequence of an isolated nuclear action comparising at least to the Sequence of an isolated nuclear action of the comparising at least to the Sequence of the Sequence P450 A1 (CYP4501A1), evrochrome P450 A2 (CYP4501A2), ary prochrome P450 O2B1 (CYP4501A1), ary and acceptor nuclear translocator (ARM), aryl hydrocarbon receptor nuclear translocator (ARM), cathepain S (CYPS), cycloxogenaes 2 (COX2), diazepam binding inhibitor (DB1), epoxide hydrocarbon receptor nuclear translocator (ARM), cathepain S (CYPS), cycloxogenaes 2 (COX2), diazepam binding inhibitor (DB1), epoxide hydrocarbon receptor nuclear translocator cathefarse (HMMT), (Kallikrein 2) KLK2, incolinamide -N-methyl transferase (HMMT), Lactorransferase thermolabile (STM), UDP-glucuronosyl transferase 2B4 (UGT2B1), unckinase receptor (URP), multidrug resistance 1 (MRP3), actorransferant receptor (MRII2), or acctylcholine muscathinc (MRP3), orphan nuclear receptor (MRII2), or acctylcholine muscathinc creeptor 1, 2, 3, 4, or 5 (CHWRI, CHWR2, CHWR3, CHWR4 or CHWR5) sequence (GRP3), orphan nuclear receptor (MRII2), or acctylcholine muscathing and characterising the genes tesponsible for specific traits within the genome and eventually identifying the genes responsible for a variety of disorder-related traiting as a result of their e.g., overexpression, mutation or underexpression, which may be used in disonsing and/or treating the disorders. The nucleic acid molecules comprising the corpusing the disorders. The nucleic acid molecules comprising the corpusing the disorders. The nucleic acid molecules comprising the corpusing the engagences contained in CYP4501A1, CYP4501A Isolated nucleic acid molecules having polymorphisms in known human genes e.g. cytochrome p450 and cathepsin S useful as genetic linkage markers for locating, identifying and characterizing the genes responsible for Gaps This invention relates to the sequence of an isolated nucleic acid ö 0.4%; Score 16.4; DB 1; Length 20; 14.4%; Pred. No. 1.1e+03; 1; Indels Sequence 20 BP; 10 A; 8 C; 0 G; 2 T; 0 U; 0 Other; 0; Mismatches Example 16; Page 131; 714pp; English 2315 Grendrerergrerer 2332 18 Grardrererererer 1 28-NOV-2001; 2001WO-US044838. 28-NOV-2000; 2000US-00724389 Query Match 0.4%; Best Local Similarity 94.4%; Matches 17; Conservative disorder-related traits. (DNAS-) DNA SCI LAB INC WPI; 2002-698522/75. Hall J; WO200257410-A2. 25-JUL-2002. Guida M, ð

vivlemore401-10.rng

sapiens

Length 20;

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Seguence 20 BP; 6 A; 5 C; 5 G; 4 T; 0 U; 0 Othér;
                                                          WO2003025144-A2
                              nodified_base
                                       modified base
                                               modified base
      01-JUL-2003
                                                              27-MAR-2003
                         Synthetic.
                                                                                             disorders.
  ACC49689;
                                                                               Monia
                       Homo
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BP,

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VEGFR-2 antisense oligonucleotide #42.
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                                                                                      1672 ATCGCAGACTTCGGGCTG 1689
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                                                                                                                                                                                                                                    BP
0.4%;
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                                                                                                               20 ATCACAGACTTCGGGCTG
                                                                                                                                                                                                                                    ACC80119 standard; DNA; 20
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                                             17; Conservative
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                     Best Local Similarity Matches 17; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     modified base
                                                                                                                                                                                                                                                                                                                   01-AUG-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10-APR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Synthetic.
                                                                                                                                                                                                                                                                             ACC80119;
        Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention describes a compound 8-50 nucleobases in length targeted to, and which specifically hybridises with a nucleic acid molecule encoding kinase suppressor of ras-1 (KRR), and inhibits the expression of KSR. Also described: (1) a compound 8-50 nucleobases in length that specifically hybridises with at least an 8-nucleobase portion of an ancies and anolecule encoding KSR; (2) a composition comprising the compound and a carrier or diluent; (2) a composition comprising the compound and a carrier or diluent; (2) a composition comprises with the compound and acarrier or diluent; (3) to inhibiting the expression of KSR in cells or tissues by contacting the calls or tissues by the the compound so that expression of KSR is inhibited; and (4) treating an animal having a disease or condition associated with KSR by administering to the animal a therapeutic or prophylactic compound has cytostatic activity and can be used as a KSR inhibitor, and in antisense gene therapy. The compound, composition and methods are in antisense gene therapy. The compound, composition and methods are byperproliferative or developmental disorder, or a disease or condition arising from aberrant apoptosis by inhibiting the expression of KSR. They are also useful in research and diagnostics for modulating the expression of KSR. They are also useful in research and diagnostics for modulating the expression of KSR. They are also useful in research and diagnostics for modulating the expression of KSR. They are also or condition and methods are an early sequence represents a chimeric phosphorothicate
                                                                                                                                                Human; kinase suppressor of ras-1; KSR; cytostatic; KSR inhibitor; antisense gene therapy; hyperproliferative disorder; phosphorothioate; developmental disorder; antisense oligonucleotide; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  compounds, particularly antisense oligonucleotides targeted to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     nucleic acid encoding KSR, useful for treating a disease/condition associated with KSR, such as hyperproliferative or developmental
                                                                                                           Human KSR chimeric phosphorothioate oligonucleotide SEQ ID NO:59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /mod_base= OTHER
/note= "2'-0-methoxyethyls (2'-MOE)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "2'-O-methoxyethyls (2'-MOE) 16. .20
                                                                                                                                                                                                                                                                                                                                                                                /note= "phosphorothioate backbone"
                                                                                                                                                                                                                                                                                                Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                               OTHER
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                                                                  (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New compounds, particularly antisense oligonucleotides targeted to a nucleic acid encoding vascular endothelial growth factor receptor-2 (VEGFR-2), useful for treating a disease/condition associated with VEGFR-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /mod_base= OTHER
/note= "This oligonucleotide has a phosphorothicate
backbone and 2-'methyoxyethyl (2'-MOE) wings at the 5'
and 3' ends, which are 5 nucleotides in length. Also all
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human, vascular endothelial growth factor receptor-2, cytostatic; angiogenic; antiangiogenic; antiarthritic; antirheumatic; antisense; VEGFR-2; hyperproliferative disorder; cancer; rheumatoid arthritis; angiogenesis; phosphorothloate; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              and 3' ends, which are 5 nucleotides in cytidine residues are 5-methylcytidines"
Score 16.4; DB 1;
Pred. No. 1.1e+03;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Seguence 20 BP; 5 A; 8 C; 3 G; 4 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1584 GGGCATGGAGTACTTGGC 1601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ~
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ð
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The invention relates to a novel polynucleotide isolated and purified from a human gene having any one of 935 fully defined sequences as given in specification, or a sequence having a base substitution. The invention further relates to: an oligonucleotide containing single nucleotide polymorphisms; a PCR primer set chosen from the combination of two DNA fragments from any one of 1220 fully defined sequences as given in specification; a labelling probe containing the SNP containing oligo; and a microarray equipped with the SNP containing oligo. The isolated human gene of the invention is useful for detecting the single nucleotide polymorphisms in human gene. The isolated human gene is also useful for diagnosis of disease and determination of side effect to a medical agent. The isolated human gene is also effective in detecting single nucleotide polymorphisms in a human gene. This polymocleotide sequence represents one of the PCR primers used in the single nucleotide polymorphism
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   polynucleotide useful for detecting single nucleotide polymorphisms
                                                                                                                                                                                    human; single nucleotide polymorphism; microarray; side effect; ss;
                                                                                                                                                     Single nucleotide polymorphism detection primer, SEQ ID No 1427.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 20 BP; 8 A; 8 C; 4 G; 0 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 2; SEQ ID NO 1427; 704pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  detection method of the invention.
                                     ADF87844 standard; DNA; 20 BP
                                                                                                                                                                                                                                                                                                                                                                                                                     12-FEB-2002; 2002JP-00034717.
                                                                                                                                                                                                                                                                                                                                                                                  12-FEB-2002; 2002JP-00034717
                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2003-820454/77
                                                                                                                                                                                                                                                                                                      JP2003235571-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         human gene.
                                                                                                                                                                                                                                                                    Homo sapiens.
                                                                                                               26-FEB-2004
                                                                                                                                                                                                                                                                                                                                             26-AUG-2003
                                                                                                                                                                                                           primer; PCF
                                                                                                                                                                                                                                                 Synthetic.
                                                                          ADF87844;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel
RESULT 888
ADF87844/c
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an isolated nucleic acid probe or primer comprising at least 8 configuous nucleotides of the nucleic acid, an isolated antisense nucleic acid, didentifying an AbAM or interactor gene ligand and an isolated nucleic acid variant of Gene 803, 845, 847, 874 or 962. The nucleic acid or alternate splice variants, methods, kits and antibody/antibody fragment are useful for diagnosing and treating an ADAM or interactor geneassociated disorder, e.g. asthma, atopy, obesity or inflammatory bowel disease. The present sequence is an SSCP (single-strand conformation polymorphism) primer used to analyse the above genes for the presence of ô Gaps ö Score 16.4; DB 1; Length 20; Pred. No. 1.1e+03; 0; Mismatches 1; Indels 2344 ~ 94.48; 2327 GTGTGTGCGTGTGTGT **crererecerererer** ADP75264 standard; DNA; 20 (first entry) 17; Conservative Query Match Best Local Similarity 12-AUG-2004

13

a ઠ

Matches

RESULT 889

Human; SSCP; 88; primer; ADAM19; Endophilin 1; Endophilin 2; NRG2;

Human NRG2 gene exon A SSCP reverse primer #1.

ADP75264;

ADP75264/6
ID ADP77
XX
AC ADP77
XX
DT 12-A
XX
XX
KW Huma

The invention relates to an isolated nucleic acid or alternate splice variant comprising a nuclectide sequence containing at least one of the cangle in the nuclectide polymorphisms given in the specification, a nuclectide sequence having at least 15 contiguous nuclectides of them, or complements of them. The genes are ADAM19 (a disintegrin and metalloprotease 19, also known as gene 845), NRG2 (neuroregulin 2, also known as gene 845), NRG2 (neuroregulin 2, also known as gene 845), NRG2 (neuroregulin 2, also known as gene 861) and ADAM752 (a disintegrin and metalloprotease with thrombospondin typel motif 2, also known as gene 874), endophilin 2 are a vector comprising the isolated nucleic acid (or alternate splice with thrombospondin typel motif 2, also known as gene 871), and nucleic acid (or alternate splice variant), a host cell containing the vector, an isolated polypeptide or antibody or antibody reagment that binds to the polypeptide.

Contained by the novel nucleic acid (or alternate splice variant, vector, polypeptide or antibody, and a carrier, plant or alternate splice variant binds to the polypeptide.

Contained at least one component to detect the hybridisation of the variant or the binding of the antibody to an ADAM gene mucleotide sequence (comprising the metalloprotease (ADAM) gene nucleotide sequence (comprising the antibody or antibody to the interactor gene amino acid sequence), a kit of detecting an interactor gene amino acid sequence), and the binding of the antibody to the interactor gene amino acid sequence), and indiagody to the interactor gene amino acid sequence), and respiratory disorder in a human subject, determining an ADAM or interactor gene pharmacogenetic profile in a human subject, identifying an orthologue of a human ADAM or interactor gene amino acid sequence.

Confidence of a human ADAM or interactor gene amino acid sequence comprises an introduced null mutation in an endogenous genice comprises an introduced null mutation in an endogenous sequence comprises an introduced null ADAWTS2; a disintegrin and metalloprotease; neuroregulin 2; SNP; single nuclectide polymorphism; a disintegrin and metalloprotease with thrombospondin typel motif 2; asthma; atopy; obesity; inflammatory bowel disease; respiratory disorder; single-strand conformation polymorphism. New isolated nucleic acid or alternate splice variant, useful for diagnosing and treating a disintegrin and metalloprotease (ADAM) or interactor gene-associated disorder, e.g. asthma, atopy, obesity or Del Mastro RG; Dupuis J, Little RD, Van Eerdewegh P, Claim 2; Page 124; 338pp; English. (GENO-) GENOME THERAPEUTICS CORP. 11-OCT-2001; 2001US-0328424P. 11-OCT-2002; 2002WO-US032700 inflammatory bowel disease WPI; 2003-381712/36. WO2003031594-A2. Homo sapiens. 17-APR-2003. Keith T, Allen K;

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microsomal prostaglandin E2 synthase, mPGES-1; mPGES-1 inhibitor; microsomal prostaglandin E2 synthase inhibitor; cytostatic; antidiabetic; immunomodulator; cardiant; neuroprotective; antiinflammatory; neuroprotective; noctropic; antiarthritic; vasotropic; ophthalmological; immunomodulatory; cardiovasculàr; gene therapy; inflammation; Albabene; Albabene; cancer; ischaemia; reperfusion injury; ophthalmic disorder; immunological disorder; acridiovascular disorder; neurological disorder; se.
                                                                                                                                                                                                                                                                                                                                                                                           25-SEP-2002; 2002US-0413549P.
                                                                                                                                                                                                                                                                                                                                                                    25-SEP-2003; 2003WO-US030374.
                                                                                                                                                                                                                                                                                                                                                                                                                  (PHAA ) PHARMACIA CORP
                                                                                                                                                                                                                                                                                                                      WO2004028458-A2
                                                                                                                                             Key
modified_base
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                                                                                                                                                                                                                                                                                                                                              08-APR-2004
                                                                                                                       Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                         Gierse JK;
                                                                                                            Ношо
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention relates to a polynucleotide isolated from a human gene and is useful for detecting a single nucleotide polymorphism in a human gene or for diagnosing of disease. The invention enables the detection of a single nucleotide polymorphism in a human gene. The present sequence represents a primer of the invention.
                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel polynucleotide useful for PCR amplification along with two DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           fragment from another set of sequences, or for detecting single nucleotide polymorphism in human gene.
                                                                          .;
0
                                             Query Match 0.4%; Score 16.4; DB 1; Length 20; Best Local Similarity 94.4%; Pred. No. 1.1e+03; Matches 17; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0.4%; Score 16.4; DB 1; Length 20; 94.4%; Pred. No. 1.1e+03; tive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                           human; single nucleotide polymorphism; SNP; ss; primer.
                            Sequence 20 BP; 6 A; 2 C; 8 G; 4 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 20 BP; 6 A; 5 C; 6 G; 3 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 2; SEQ ID NO 5935; 2627pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                  (KAGA-) KAGAKU GLJUTSU SHINKO JIGYODAN
                                                                                                2632 CCACATGTCCAGCACCTT 2649
                                                                                                              20 CCACTTGTCCAGCACCTT 3
                                                                                                                                                                                ADK96906 standard; DNA; 20 BP.
                                                                                                                                                                                                                                                   Primer of the invention #2626
                                                                                                                                                                                                                                                                                                                                                                     08-MAR-2002; 2002JP-00064373
                                                                                                                                                                                                                                                                                                                                                                                            08-MAR-2002; 2002JP-00064373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity 94.4 es 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2004-093977/10.
                                                                                                                                                                                                                                                                                                                        JP2003259875-A.
   polymorphisms
                                                                                                                                                                                                                            06-MAY-2004
                                                                                                                                                                                                                                                                                                                                               16-SEP-2003.
                                                                                                                                                                                                                                                                                                  Synthetic
                                                                                                                                                                                                      ADK96906;
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Matches
                                                                                                                                                        SXS
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/note= "phosphorothioate linkages and all cytidine residues are 5-methylcytidines"

Location/Qualifiers

sapiens

/mod_base= OTHER

/*tag= a /mod_base= OTHER /note= "2'-O-methocyethyls" 16. .20

 $'not\overline{e}= "2'-0-methoxyethyls"$

/*tag= c /mod_base= OTHER

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                                                                                                                                                                                                                                                                                                                                                                                                                             The present sequence represents a chimeric antisense oligonucleotide targeted to human microsomal prostaglandin E2 synthase (mpGES-1). The human mpGES-1 gene is located on chromosome 9, more specifically to 9d34.3. The present invention also describes: (1) antisense compounds, having a sequence comprising 8-30 bp targeted to a nucleic acid encoding mpGES-1, which specifically hybridise with the nucleic acid mpGES-1 and inhibits its expression; (2) a method of inhibiting the expression of mpGES-1 in cells or tissues; and (3) a method of treating an animal having a disease or condition associated with mpGES-1. MpGES-1 chimeric antidiabetic, immunomodulator, cardiant, neuroprotective, antidiabetic, immunomodulator, cardiant, neuroprotective, antidiated can ophthalmological, immunomodulatory and cardiovascular activities, cand can ophthalmological, immunomodulatory and cardiovascular activities, and candidona.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ischaemia or reperfusion injury, or lar or neurological disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           be used as mPGES-1 inhibitors and in gene therapy. The antisense compound can be used for preparing a composition for treating a disease or condition associated with mPGES-1 e.g., inflammation, Alzheimer's
                                                                                           New antisense compound, having a sequence targeted to a nucleic acid encoding mPGES-1, useful for preparing a composition for treating e.g., inflammation, Alzheimer's disease, arthritis, diabetes, cancer or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ..
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 20 BP; 8 A; 8 C; 2 G; 2 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ophthalmic, immunological, cardiovascular or
                                                                                                                                                                                                                                                                                                                                                Claim 4; SEQ ID NO 1098; 132pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          diabetes, cancer,
WPI; 2004-305094/28.
                                                                                                                                                                                                                                                          ischemia.
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Gaps

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327 CICCAICICCIGGCIGAA 344

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20 CTCCATCTGCTGGCTGAA

ADM14911 standard; DNA; 20

Human mPGES-1 chimeric antisense oligonucleotide SEQ ID NO:1098

(first entry)

01-JUL-2004

ADM14911;

chimeric; antisense oligonucleotide; phosphorothioate; human;

Genetic proximity, gene expression; cell characterisation; homeobox gene; genetic defect; reverse transcriptase polymerase chain reaction; RT-PCR; kinase gene; protein phosphatase; P450; steroid receptor; cadherin;

PTK 28 gene specific primer.

11-OCT-1999 (first entry)

AAZ18186;

98WO-IL000625. 97IL-00122793. 98IL-00126627.

28-DEC-1998;

08-JUL-1999

Homo sapiens. W09934016-A2

primer; ss Synthetic.

AAZ18186 standard; DNA; 21 BP.

RESULT 893

4AZ18186,

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The invention provides a new method for identifying and characterising cells. The method for determining the genetic proximity of a first cell and a day accord cell comprises: (a) obtaining the first cell and the second cell the pattern of expression of genes in a selected gene family; and (c) calculating a proximity index using a specified formula. The methods can be used for characterising cells, e.g. for determining the origin of a cell, its. Genetic status, whether it carries a genetic defect, or whether it is transformed. They can be used for detecting a selected genetic defect in an individual, e.g. a fetus. They can also be used for determining the effect of a selected treatment on a test cell. They can also be used for obtaining cells capable of expressing an homeobox related desired property. The method uses reverse transcriptase polymerase chain reaction containing. Sequences AAZI7803-Z18342 represent primers that can be used gene family. Sequences AAZI7803-Z18342 represent primers that can be used in the RT-PCR reactions to determine the pattern of gene expression. The gene family can be selected from a set of homeobox genes, characteristic and the property of the pattern of gene expression. The containing cells capable of the pattern of gene expression. The containing cells capable of the pattern of gene expression. The containing cells capable of the pattern of gene expression. The containing cells capable of the pattern of gene expression. The containing cells capable of the pattern of gene expression and the containing cells capable of the containing cells capable of the capable of the pattern of gene expression. The containing cells capable of the capab
                                                                                                                                                                                                                                                                                                                                                                                 Genetic proximity; gene expression; cell characterisation; homeobox gene; genetic defect; reverse transcriptase polymerase chain reaction; RT-PCR; kinase gene; protein phosphatase; P450; steroid receptor; cadherin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Identifying and characterizing cells by comparing the pattern of gene expression in a selected gene family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein phosphatase genes, P450 enzyme genes, steroid receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0.4%; Score 16.4; DB 1; Length 21;
94.4%; Pred. No. 1.2e+03;
ve 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 21 BP; 7 A; 8 C; 4 G; 2 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 superfamily genes or cadherin superfamily genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 4; Page 46; 102pp; English.
2316 rererererererere 2333
                          18 rccgrgrgrgrgrgrg 1
                                                                                                                                                                               BP
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98IL-00126627
                                                                                                                                                                                                                                                                                                                                   PTK 25 gene specific primer.
                                                                                                                                                                               AAZ18180 standard; DNA; 21
                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1999-419113/35.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (GENE-) GENENA LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P-PSDB; AAY14715
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO9934016-A2.
                                                                                                                                                                                                                                                                                11-OCT-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29-DEC-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Synthetic.
                                                                                                                                                                                                                               AAZ18180;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Vider B;
                                                                                                                            RESULT 892
                                                                                                                                                         AAZ18180,
                                                                                                                                                                               8
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Identifying and characterizing cells by comparing the pattern of gene expression in a selected gene family.

NPI; 1999-419113/35.

Vider B;

P-PSDB; AAY14721

(GENE-) GENENA LTD

16-OCT-1998; 29-DEC-1997;

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The invention provides a new method for identifying and characterising cells. The method for determining the genetic proximity of a first cell and a second cell comprises: (a) obtaining the first cell and the second cell; (b) determining in the first cell and the second cell; (b) determining in the first cell and the second cell; (b) determining in a selected gene family; and (c) calculating a proximity index using a specified formula. The methods can be used for characterising cells, e.g. for determining the origin of a cell, its genetic status, whether it carries a genetic defect, or whether it is transformed. They can be used for determining the condividual, e.g. a fecus. They can also be used for determining the effect of a selected treatment on a test cell. They can also be used for obtaining cells capable of expressing an homeobox related desired property. The method uses reverse transcriptase polymerase chain reaction (RT-PCR) for determining the pattern of gene expression in a selected gene family. Sequences AA17803-21842 represent primers that can be used in the RT-PCR reactions to determine the pattern of gene expression. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gene family can be selected from a set of homeobox genes, kinase genes,
protein phosphatase genes, P450 enzyme genes, steroid receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 21 BP; 7 A; 8 C; 4 G; 2 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        superfamily genes or cadherin superfamily genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 4; Page 46; 102pp; English.
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les 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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0XCCCCCCCCCCCCCCCCX8X414X88X1X8X6X6X6X6X8X8X8X8X8X8X8X8X8X8X8
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RESULT 894

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Gaps ö

1801 GACGTCTGGTCCTTTGGG 1818

94.48;

17; Conservative

Matches

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Local Similarity

GACGIGIGGICCTTIGGG 1

18

(first entry)

vivlemore401-10.rng

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Genetic proximity, gene expression, cell characterisation, homeobox gene, genetic defect, reverse transcriptase polymerase chain reaction, RT-PCR, kinase gene, protein phosphatase, P450, steroid receptor, cadherin,
                                                                                                                                                                                                                                                                                                                                                                                                                                        Identifying and characterizing cells by comparing the pattern of gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                         expression in a selected gene family.
                                                         PTK 19 gene specific primer
                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1999-419113/35.
P-PSDB; AAY14705.
                                                                                                                                                                                                                                                                                                                                       (GENE-) GENENA LTD
                                                                                                                                                                            Homo sapiens.
                                                                                                                                                                                                      WO9934016-A2
                                                                                                                                                                                                                                                                28-DEC-1998;
                                                                                                                                                                                                                                                                                           29-DEC-1997;
16-OCT-1998;
                            11-OCT-1999
                                                                                                                                                                                                                                   08-JUL-1999
                                                                                                                                  primer; ss
                                                                                                                                                             Synthetic.
 AAZ18170;
                                                                                                                                                                                                                                                                                                                                                                    Vider B;
 The invention provides a new method for identifying and characterising cells. The method for determining the genetic proximity of a first cell and a second cell comprises: (a) obtaining the first cell and the second cell; (b) determining in the first cell and the second cell; (b) determining in the first cell and the second cell; (b) determining in the first cell and the second cell; (b) determining in a selected gene family; and (c) calculating a proximity index using a specified formula. The methods can be used for characterising cells, e.g. for determining the origin of a cell, its genetic status, whether it carries a genetic defect, or whether it is transformed. They can be used for determining the effect of a selected treatment on a test cell. They can also be used for obtaining cells capable of expressing an homeobox related desired property. The method uses reverse transcriptase polymerase chain reaction (RT-PCR) for determining the pattern of gene expression in a selected gene family. Sequences AA217803-218342 represent primers that can be used in the RT-PCR reactions to determine the pattern of gene expression. The
                                                                                                                             Genetic proximity, gene expression; cell characterisation; homeobox gene; genetic defect; reverse transcriptase polymerase chain reaction; RT-PCR; kinase gene; protein phosphatase; P450; steroid receptor; cadherin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               family can be selected from a set of homeobox genes, kinase genes,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Identifying and characterizing cells by comparing the pattern of gene expression in a selected gene family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              protein phosphatase genes, P450 enzyme genes, steroid receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Match 0.4%; Score 16.4; DB 1; Length 21; Local Similarity 94.4%; Pred. No. 1.2e+03; es 17; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 21 BP; 7 A; 8 C; 4 G; 2 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            superfamily genes or cadherin superfamily genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 4; Page 46; 102pp; English.
               AAZ18176 standard; DNA; 21 BP
                                                                                                                                                                                                                                                                                                          98WO-IL000625
                                                                                                                                                                                                                                                                                                                                       97IL-00122793
                                                                                                                                                                                                                                                                                                                                                      98IL-00126627
                                                                                                    PTK 22 gene specific primer
                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1999-419113/35.
                                                                                                                                                                                                                                                                                                                                                                                  (GENE-) GENENA LID.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          P-PSDB; AAY14711
                                                                                                                                                                                                                       Homo sapiens.
                                                                        11-OCT-1999
                                                                                                                                                                                                                                                    WO9934016-A2
                                                                                                                                                                                                                                                                                                          28-DEC-1998;
                                                                                                                                                                                                                                                                                                                                         29-DEC-1997;
                                                                                                                                                                                                                                                                                                                                                        16-OCT-1998;
                                                                                                                                                                                                                                                                               08-JUL-1999.
                                                                                                                                                                              primer; ss.
                                                                                                                                                                                                        Synthetic
                                           AAZ18176;
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                                                                                                                                                                                                                                                                                                                                                                                                              Vider B;
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97IL-00122793. 98IL-00126627. 98WO-IL000625

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The invention provides a new method for identifying and characterising cells. The method for determining the genetic proximity of a first cell and a second cell comprises: (a) obtaining the first cell and the second cell the pattern cell; (b) determining in the first cell and the second cell the pattern of expression of genes in a selected gene family; and (c) calculating a proximity index using a specified formula. The methods can be used for characterising cells, e.g. for determining the origin of a cell, its constitute, whether it carries a genetic defect, or whether it is transformed. They can be used for determining the crimic status, whether it carries a genetic defect, or whether it is considered. They can also be used for a individual, e.g. a fetus. They can also be used for determining the ceffect of a selected treatment on a test cell. They can also be used for obtaining cells capable of expressing an homeobox related desired considering the pattern of gene expression in a selected considered from a set of homeobox genes that can be used con the family. Sequences AAZ17803-Z18342 represent primers that can be used con the family can be selected from a set of homeobox genes, kinase genes, protein phosphatase genes, P450 enzyme genes, steroid receptor considering upperfamily genes or cadherin superfamily genes
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14.4%; Pred. No. 1.2e+03;
ve 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 21 BP; 7 A; 8 C; 4 G; 2 T; 0 U; 0 Other;
Claim 4; Page 46; 102pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1801 GACGTCTGGTCTTTGGG 1818
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ВЪ.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 94.4%;
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAZ18192 standard; DNA; 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11-OCT-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAZ18192;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ouery Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 896
AAZ18192/c
ID AAZ1815
XX
AC AAZ1815
XX
DY 11-OCT-
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Gaps ; 0

1801 GACGTCTGGTCCTTTGGG 1818

Best Loca Matches

18 caccicicitoricitices

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AAZ18170/c ID AAZ18170 standard; DNA; 21 BP. XX

RESULT 895

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Genetic proximity, gene expression, cell characterisation, homeobox gene; genetic defect, reverse transcriptase polymerase chain reaction, RT-PCR, kinase gene; protein phosphatase; P450, steroid receptor; cadherin;
                                                                                                                                                                                                        Identifying and characterizing cells by comparing the pattern of gene expression in a selected gene family.
                                                                                                                                                                                                                                Claim 4; Page 47; 102pp; English
       PTK 32 gene specific primer.
                                                                                                                                                                                   WPI; 1999-419113/35
                                                                                                                                                     (GENE-) GENENA LTD
                                                                                                                                                                                           P-PSDB; AAY14727
                                                                  Homo sapiens
                                                                                 WO9934016-A2
                                                                                                               28-DEC-1998;
                                                                                                                                     16-OCT-1998;
                                                                                                                             29-DEC-1997;
                                                                                                 08-JUL-1999
                                            primer; ss
                                                           Synthetic
                                                                                                                                                                    Vider B;
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The invention provides a new method for identifying and characterising cells. The method for determining the genetic proximity of a first cell and a second cell comprises: (a) obtaining the first cell and the second cell; (b) determining in the first cell and the second cell; (b) determining in the first cell and the second cell; (b) determining in the first cell and the second cell; (b) determining a selected gene family; and (c) calculating a proximity index using a specified formula. The methods can be used for characterising cells, e.g. for determining the origin of a cell; its genetic status, whether it carries a genetic defect, or whether it is transformed. They can be used for determining the effect of a selected treatment on a test cell. They can also be used for obtaining cells capable of expressing an homeobox related desired cobtaining cells capable of expressing an homeobox related desired (RT-PCR) for determining the pattern of gene expression in a selected gene family. Sequences ARZH303-ZH3942 represent primers that can be used in the RT-PCR reactions to determine the pattern of gene expression. The genes, kinase genes, Gaps ; 0 gene family can be selected from a set of homeobox genes, kinar protein phosphatase genes, P450 enzyme genes, steroid receptor superfamily genes or cadherin superfamily genes Score 16.4, DB 1; Length 21; Pred. No. 1.2e+03; 0; Mismatches 1; Indels Sequence 21 BP; 7 A; 8 C; 4 G; 2 T; 0 U; 0 Other; Query Match

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1801 GACGTCTGGTCCTTTGGG 1818
Best_Local Similarity 94.4%;
Matches 17; Conservative
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18 caccigiratericerriese

AAC69306 standard; DNA; 21 BP AAC69306

RESULT 897 AAC69306 (first entry) 29-JAN-2001 Human ABC1 gene promoter polymorphic site, SEQ ID NO:205.

Human ABC1 cholesterol transporter; chromosome 9q31; ATP-binding cassette; HDL deficiency disorder; high density lipoprotein; Tangier disease; TD; familial HDL deficiency; FHA; polymorphism; cerebrovascular disease; peripheral vascular disease;
Alzheimer's disease; Niemann-Pick disease; Huntington's disease;
X-linked adrenoleukodystrophy; cancer; gene therapy; genetic diagnosis; prophylaxis; drug screening; transgenic animal; ds. cardiovascular disease; coronary artery disease; coronary restenosis;

Homo sapiens.

WO200055318-A2.

21-SEP-2000

15-MAR-2000; 2000WO-IB000532.

98WO-IL000625. 97IL-00122793. 98IL-00126627.

99US-0138048P. 99US-0139600P. 99US-0151977P. 17-JUN-1999; 01-SEP-1999; LS-MAR-1999; 18-JUL-1999;

(UYBR-) UNIV BRITISH COLUMBIA (XENO-) XENON BIORESEARCH INC

Hayden MR, Wilson AR, Pimstone SN;

WPI; 2000-587528/55

New ABC1 polypeptide is useful for treating diseases associated with ABC1 biological activity, e.g. Alzheimer's disease, Huntington's disease and

Example; Fig 11; 229pp; English

The invention relates to the human ABC1 cholesterol transporter protein (B38082) and to nucleic acid sequences (C69120) which encode it. ABC1 is a member of the ATP-binding cassette (ABC transporter) superfamily of proteins, and plays a crucial role in Cholesterol transport, particularly intracellular cholesterol efflux from the cell. The gene encoding ABC1 is involved in cholesterol efflux from the cell. The gene encoding ABC1 is corated on chromosome 9431, and mutations in this gene are associated with two genetic HDL (high density lipoprotein) deficiency (FHA). These diseases of the standinable in that TD is an autosomal recessive disorder, while FHA is inherited as an autosomal adminant trait. Low levels of HDL ("good cholesterol") in the blood correlate with a high risk of cardiovascular cisease, particularly coronary artery disease, but also cerbrovascular disease. Coronary restenois, and peripheral vascular disease compounds for the treatment or prevention of cardiovascular disease compounds which minmic ABC1 activity, compounds which minmic ABC1 activity, compounds which attended to encompasses compounds which minmic ABC1 activity, compounds which attended to restend to the invention of cardiovascular disease, especially coronary artery disease, coronary restenois or peripheral vascular disease, coronary restenois or peripheral vascular disease, coronary restenois or peripheral vascular disease. The proteins and nucleotides can be used to treat or prevent cardiovascular disease, especially coronary artery disease, coronary restenois or peripheral vascular disease, coronary restenois or peripheral vascular disease, coronary restenois or peripheral vascular disease, coronary restenois or peripheral values and disease. They may also be used in the treatment of diseases associated disease. The invention specifically excludes proteins with the exact amino acid sequences of GenBank Accession No: CAA10005.1 and X75956, and the nucleic acid with the exact sequence as GenBank Accession No: AJ012376.1. The present sequence represents a polymorphic site of the human ABC1 gene disease, Huntington's disease, X-linked adrenoleukodystrophy and cancer.

Sequence 21 BP; 2 A; 6 C; 9 G; 4 T; 0 U; 0 Other;

Query Match

0.4%; Score 16.4; DB 1; Length 21;

Matches

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The present invention relates to a method for treating a patient diagnosed as having a lower than normal high density lipoprotein-cholesterol (HDL-C) level, a higher than normal triglyceride level, or a cardiovascular disease, involving administering a compound that modulates LXR- or RXR-mediated transcriptional activity or ABC1 expression or activity. The LXR gene product may be used in an assay to identify compounds useful for the treatment of a disease or condition selected a lower than normal HDL cholesterol level, a higher than normal triglyceride level, and a cardiovascular disease
                                                                                                                                                                                                                                                                                                                                                                              Treating a lower than normal high density lipoprotein-cholesterol (HDL-C) level, a higher than normal triglyceride level, or a cardiovascular disease, by administering a compound that modulates LXR- or RXR-mediated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; single nuclectide polymorphic; SNP; forensic science; paternity testing; phenotypic trait; genetic mapping; animal breeding; plant breeding; ds.
                                                                    High density lipoprotein-cholesterol; HDL-C; cardiovascular; ABCl; ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 16.4; DB 1; Length
Pred. No. 1.2e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human polymorphic oligonucleotide U63963 fragment #13
                                                                                                                                                                                                                                                                                                                         Pimstone SN, Clee SM;
                                         Polymorphic sequence for ABC1 polymorphic site #18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 21 BP; 2 A; 6 C; 9 G; 4 T; 0 U; 0 Other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
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11
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Fig 4; 317pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 ACACGCTGGGCGTGCTGG 18
                                                                                                                                                                                                                                                                                (UYBR-) UNIV BRITISH COLUMBIA
                                                                                                                                                                                                                                                                                                                          Hayden MR, Brooks-Wilson AR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BP
                                                                                                                                                                                        01-SEP-2000; 2000WO-IB001492.
                                                                                                                                                                                                                      99US-0151977P
                                                                                                                                                                                                                                   .5-MAR-2000; 2000US-00526193.
                                                                                                                                                                                                                                                   23-JUN-2000; 2000US-0213958P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0.4%;
Local Similarity 94.4%;
les 17; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            497 ACACGCTGGACGTGCTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAH89131 standard; DNA; 21
                                                                                                                                                                                                                                                                                               (XENO-) XENON GENETICS INC
             17-MAY-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (revised)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                              transcriptional activity
                                                                                                                                                                                                                                                                                                                                                       WPI; 2001-244356/25.
                                                                                                                                WO200115676-A2,
                                                                                                                                                                                                                      01-SEP-1999;
                                                                                                    Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unidentified
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                                                                                                                                                             08-MAR-2001.
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27-FEB-2002
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variation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention relates to loblolly pine polynucleotides with one or more Simple Sequence Repeats (SSRs) (see AAA74205-A74322). SSRs are also known as microsatellite DNA repeats. The SSRs are useful as genetic markers for genetic mapping, population genetics studies and inheritance studies in various plant breeding programmes. The present sequence is a PCR primer used for detecting the presence of a SSR locus in a pine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Polynucleotide having simple sequence repeat useful as markers in plants for genetic characterization e.g. genetic mapping study, an inheritance study of a commercially important trait in a plant breeding program.
                                                                                                                                                                                                                                                                              PCR primer; loblolly pine; Simple Sequence Repeat; SSR; microsatellite DNA repeat; genetic marker; mapping; inheritance study; population genetics study; plant breeding programme; ss.
                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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94.4%; Pred. No. 1.2e+03;
ive 0; Mismatches 1; Indels
Pred. No. 1.2e+03;
                                                                                                                                                                                                                                                   Forward PCR primer for loblolly pine locus RIPPT11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Seguence 21 BP; 2 A; 6 C; 4 G; 9 T; 0 U; 0 Other;
                             0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6; Page 21; 57pp; English.
                                                        514
                                                                                     1 AcAcecrasecerecines 18
                                                                                                                                                              BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           99US-00232884
99US-00232785
               94.48;
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17; Conservative
                                                          497 ACACGCTGGACGTGCTGG
                                                                                                                                                              AAA73573 standard; DNA; 21
                                                                                                                                                                                                                       29-NOV-2000 (first entry)
                           17; Conservative
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NELSON C D.
US SEC OF AGRIC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (INTO ) INT PAPER CO. (ECHT/) ECHT C'S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2000-482836/42.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Echt CS, Nelson CD;
               Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    genomic DNA sample
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                                       WO200042210-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                            L5-JAN-1999;
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                                                                                                                                                                                                                                                                                                                                           Pinus taeda
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18
                                                                                                                                                                                            AAA73573;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (NELS/) 1
(USDA ) 1
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AAF92948
ID AAF9294
XX
AC AAF9294
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Siegel S;

vivlemore401-10.rng

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The invention relates to a method of treating a vascular inflammatory pathology in a human, comprising administering a single or divided 0.5-15 mg/kg dose at least once every 1-6 weeks of an anti-tumour necrosis factor (TMF) chimeric antibody which competitively inhibits binding of TNF to monoclonal antibody CA2. The invention is used to treat a vascular inflammatory pathology particularly Kawasaki's pathology or disseminated intravascular coagulation or atheroselerosis. The present sequence represents DNA encoding the pLC671 partial sequence with insert #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               rheumatoid arthritis; systemic lupus erythematosus; diabetes mellitus; angiogenesis; autoimmune pathology; graft versus host disease; cachexia; scleroderma; infection; circulatory collapse; inflammatory disease; inflammatory bowel disease; neurodegenerative disease; sepsis syndrome; Crohn's disease; ulcerative collitis; multiple sclerosis; angiogenesis; lymbhoma; infantile haemangioma; alcohol-induced hepatitis; cytostatic; ocular neovascularisation; alcohol-induced hepatitis; cytostatic; immunosuppressive; neuroprotective; hepatotropic; antiangiogenic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 joint inflammation; tumour necrosis factor; TNF; joint stiffness;
                                                                                                                                                                                                                                                                                                        Treating a vascular inflammatory pathology, e.g. Kawasaki's pathology, comprises administering an anti-Tumor Necrosis Factor (TNF) chimeric antibody which competitively inhibits binding of TNF to a monoclonal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 16.4; DB 1; Length 21; Pred. No. 1.2e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Indels
                                                                                                                                                                                                                          Ghraveb J, Knight D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 21 BP; 5 A; 1 C; 8 G; 7 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; SEQ ID NO 28; 100pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               pLC871 plasmid partial DNA fragment #2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
920S-00943852.
930S-00010406.
930S-00013413.
94US-00192102.
94US-00192861.
94US-00192861.
95US-00570674.
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                                                                                                                                                                                                                          Le J, Vilcek J, Daddona P,
                                                                                                                                                    2001US-00756398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 94.4%;
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1506 CTCCTTCGACACCTGCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19 CTCCTTCAACACCTGCAA
                                                                                                                                                                                        UYNY ) UNIV NEW YORK STATE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
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Chimeric - Unidentified.
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                                                                                                                                                                                                                                                                         P-PSDB; ADD44680
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misc_feature
                                                                                                   18-OCT-1994;
11-DEC-1995;
12-AUG-1998;
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                                   02-FEB-1993
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                                                                                                                                                                                                                                                                                                                                                                antibody
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                                                                                                                                                                                                                                                                                                                                                                                                                           single nucleotide polymorphic site (SNP: AAH88797-AAH89219). The present sequence is one such oligonucleotide. The oligonucleotides can be used in forensics, paternity testing, correlation of polymorphisms with phenotypic traits, genetic mapping of phenotypic traits and marker assisted breeding of animals and crop plants
                                                                                                                                                                                                                                                                                                         New polymorphic sites derived from the human genome are useful to determine sites correlating with phenotypic traits, particularly disease, and also in forensics and paternity testing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Revised record issued on 09-SEP-2004 : Correction to Feature Table Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             human; tumour necrosis factor alpha; vascular inflammation; anti-TNF;
tumour necrosis factor; cA2; Kawasaki's pathology;
disseminated intravascular coagulation; atherosclerosis; ds; gene.
                                                                                                                                                                                                                                                                                                                                                                                                              The present invention relates to human oligonucleotides comprising a
               /standard_name= "single nucleotide polymorphism"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0.4%; Score 16.4; DB 1; Length 21;
44.4%; Pred. No. 1.2e+03;
ve 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               pLC671 partial sequence with insert #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 21 BP; 3 A; 7 C; 5 G; 6 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                          Thomas D;
                                                                                                                                                                                                                                                                                                                                                                              Claim 87; Page 14; 43pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1820 TCCTGCTCTGGGAGATCT 1837
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                                                                                                                     10-NOV-2000; 2000WO-US030766.
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                                                                                                                                                                                                                                          Patil N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity 94.4
                                                                                                                                                                                    (GLAX ) GLAXO GROUP LTD. (AFFY-) AFFYMETRIX INC.
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                                                                                                                                                                                                                                          Au K, Chen J,
                                                   WO200134840-A2
                                                                                                                                                    10-NOV-1999;
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18-MAR-1992;
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Best Loc Matches

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Gaps

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Human, ulcerative colitis, tumour necrosis factor, antiinflammatory, TNF, therapy, antiulcer, gastrointestinal, chimeric; gene; ds.

Chimeric - Homo sapiens. Chimeric - Unidentified.

Plasmid pLC871 partial DNA fragment #2,

(first entry)

12-FEB-2004

AAD63597;

ВЪ.

AAD63597 standard; DNA; 21

RESULT 90 AAD63597/

19 CTCCTTCAACACCTGCAA 2

g

/*tag= c
/*tag= c
/product= "Peptide encoded by pHC871 partial DNA
fragment"

l. .7 /*tag= a /note= "Leader intron" Location/Qualifiers

Key misc_feature

CDS

'note= "No start and stop codon"

partial

/*tag= b /note= "Encodes incomplete leader peptide" 18. .19

/*tag= d /note= "Signal peptidase cleavage site"

04-MAR-2003; 2003US-00379866.

18-MAR-1992; 11-SEP-1992; 29-JAN-1993;

US2003198641-A1

misc_feature

misc_feature

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humans. The method involves administering an anti-tumour necrosis factor (TMF) chimeric antibody or its fragment, which competitively inhibits conformed involves administering an anti-tumour necrosis factor (TMF) chimeric antibody or its fragment, which competitively inhibits binding of TNF to monoclonal antibody CA2. The anti-TNF antibodies are useful for treating joint inflammation or joint stiffness associated with creating to treat angiogenesis, such as in the treatment of a VEGF-mediated disease or to treat TNF-related pathologies such as acute and chronic cutcimmune pathologies (e.g. graft versus host disease, diabetes mellitus or solestoderma, infections (e.g. sepsis syndrome, cachexia or circulatory collapse), inflammatory disease (e.g. ulcerative colltis, inflammatory disease), neurodegenerative disease (e.g. bowel disease), antipipe sclerosis, Huntington's disease or Alzheimer's disease), multiple sclerosis, Huntington's disease or Alzheimer's disease), maltignant pathologies (e.g. lymphoma, infantile haemangioma or cancerralated angiogenesis (e.g. lymphoma, infantile haemangioma or cancerralated congiogenesis (e.g. ocular neovascularisation). The present sequence is pLG871 plasmid partial DNA fragment used in the careful construction of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Use of anti-tumor necrosis factor (TNF) chimeric antibody for treating e.g. joint inflammation or joint stiffness, infections, inflammatory diseases, neurodegenerative disease, or malignant pathologies.
                                                                                 /*tag= c
/product= "Peptide encoded by pLC871 partial DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Siegel S;
                                                "Encodes incomplete leader peptide"
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/note= "Signal peptidase cleavage site"
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                                                                                                                  fragment"
/note= "No start and stop codon"
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"Leader intron"
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92US-00853606.
92US-00010406.
93US-00013413.
94US-00192093.
94US-00192861.
94US-00122861.
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                                                                                                                                                                                                                                                                                                  2003US-00371443
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18. .19
/*tag= d
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02-FEB-1993;
04-FEB-1994;
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18-MAR-1992;
11-SEP-1992;
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The present invention relates to a method of treating ulcerative colitis in a human in need. The method involves administering a tumour necrosis factor (TNF)-inhibiting amount of an anti-TNF chimeric antibody that competitively inhibits binding of TNF to monoclonal antibody CA2. The
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Siegel
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 26; Fig 29; Opp; English.
                                                                                                                                                                                                                                                                                                           92US-00853606.
92US-001406
93US-0013413.
94US-00192102.
94US-00192861.
94US-00192861.
95US-00570674.
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Query Match 0.4%; Score 16.4; DB 1; Length 21; Best Local Similarity 94.4%; Pred. No. 1.2e+03; Matches 17; Conservative 0; Mismatches 1; Indels

1506 CTCCTTCGACACCTGCAA 1523

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Indels

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0; Mismatches

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17; Conservative
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                                                                                                                                                                                                 Unidentified
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02-FEB-1993;
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methods and compositions are useful for treating ulcerative colitis in humans. The present sequence is pLC871 plasmid partial DNA fragment used in the exemplification of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         human an
                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 antibody
                                                                                                                                                                                                                                                psoriatic arthritis; chimeric antibody; pLC671; human; ds; gene.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Treating psoriatic arthritis in a human by administering to anti-TNF chimeric antibody for a period of time, where the a inhibits binding of TNF to monoclonal antibody CA2.
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                                                       Query Match 0.4%; Score 16.4; DB 1; Length 21; Best Local Similarity 94.4%; Pred. No. 1.2e+03; Matches 17; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Seguence 21 BP; 5 A; 1 C; 8 G; 7 T; 0 U; 0 Other;
                                       Sequence 21 BP; 5 A; 1 C; 8 G; 7 T; 0 U; 0 Other;
                                                                                                                                                                                                                             pLC67I partial sequence with insert DNA #1.
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92US-00943852.
93US-00010406.
93US-00013413.
94US-00192102.
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94US-00324799.
95US-00570674.
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                                                                                                              19 CTCCTTCAACACCTGCAA
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                                                                                                                                                                    ADG27455 standard; DNA; 21
                                                                                                                                                                                                          (first entry)
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                                                                                                                                                                                                                                                                             Homo sapiens.
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04-FEB-1994;
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02-FEB-1993
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                                                                                                                                                                                                                                                                    Synthetic
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ADG27455/
   SXCCC
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Length 21;

Score 16.4; DB 1; Pred. No. 1.2e+03;

0.4%;

Query Match Best Local Similarity

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Anti-idiotypic antibodies that bind specifically to chimeric or humanized antibodies that binds to human Tumor Necrosis Factor (TNF)alpha, useful for detecting TNFalpha in samples and for diagnosing TNFalpha mediated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                           necrosis factor-alpha; TNF-alpha; pharmaceutical; diagnostic;
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Pred. No. 1.2e+03;
0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /*tag= c
/product= "pLC671 vector peptide"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "No start and stop codon"
                                                                                                                                                                                                                                                                                                                                                                               INF-mediated pathology; therapy; gene; ds
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Leader sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               a
"Leader intron"
                                                                                                                                                                                                                                                                                                            pLC671 vector peptide encoding DNA #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example XXIV; Fig 29; 90pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (UYNY-) UNIV NEW YORK MEDICAL CENT
1523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     91US-00670827.
92US-00853606.
92US-00943852.
93US-00010406.
93US-00013413.
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                                                                                                                                                              BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Le J, Vilcek J, Daddona P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2001US-00897724
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 94.4%;
Matches 17; Conservative
1506 CTCCTTCGACACCTGCAA
                                            crecrreadeacerdeaa
                                                                                                                                                              ADM83174 standard; DNA; 21
                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'partial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /*tag=
/note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note=
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P-PSDB; ADM83173.
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1584 GGGCATGGAGTACTTGGC 1601

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This invention relates to novel compositions that comprise short interfering RNA (siRNA) molecules, which can be used to inhibit can engiquenesis. Specifically, it refers to siRNAs that target and cause candidacenesis. Specifically, it refers to siRNAs that target and cause RNAi-induced degradation of mRNA from human vascular endothelial growth factor (VEGF), the VEGF receptor (FIL-1) and the FIk-1/KDR (kinase domain certain) genes, as well as mutants derived thereof. The present invention describes sense and antisense RNA strands that form an RNA duplex and condition the target mRNA, such that expression is inhibited and the target degraded. As such, siRNA administered in combination with a therapeutic agent is useful for treating disease associated with angiogenesis and the overexpression of VEGF, which include diabetic retinopathy, agence related macular degeneration, inflammatory disease, psoriasis and remanated arthritis. Furthermore, it can be used to treat various cancers including breast, retinoblastoma, Wilm's tumour and lymphoma. Accordingly, these compositions exhibit cytostatic, antidiabetic, ophthalmological, antidiabetic, antidiabetic, antidiathetic activities. This oligonuclectide is a human FIk-1/KDR DNA coligo, a target for siRNA inhibition of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel short interfering RNA (siRNA) comprises sense and antisense RNA strands, useful for inhibiting expression of human vascular endothelial growth factor mRNA, for treating angiogenic disease, e.g. diabetic
                                                                                                                                                                                                                                                                                                                      human; 88; short interfering RNA; siRNA; anglogenesis; vascular endothelial growth factor; VEGF; VEGF receptor; Flt-1; Flk-1/KDR; kinase domain region; diabetic retinopathy; age-related macular degeneration; inflammatory disease; psoriasis; rheumatoid arthritis; cancer; breast; retinoblastoma; Wilm's tumour; lymphoma; cytostatic; antidiabetic; ophthalmological; antiinflammatory; antipsoriatic; antirheumatic; antiarthritic.
                                                                                                                                                                                                                                                                               Human Flk-1/KDR DNA sequence, a target for siRNA inhibition SeqID 772.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 21 BP; 5 A; 3 C; 8 G; 5 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; SEQ ID NO 772; 218pp; English.
1506 CTCCTTCGACACCTGCAA 1523
                                      19 crecrreadacaccrecaa 2
                                                                                                                                                    BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18-JUL-2003; 2003WO-US022444.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24-JUL-2002; 2002US-0398417P.
14-NOV-2002; 2002US-00294228.
                                                                                                                                                  ADJ97999 standard; DNA; 21
                                                                                                                                                                                                                                         06-MAY-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (UYPE-) UNIV PENNSYLVANIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tolentino MJ, Reich SJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 retinopathy and cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2004-203472/19.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO2004009769-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               29-JAN-2004.
                                                                                                                                                                                               ADJ97999;
                                                                                                         RESULT 90
ADJ97999
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This invention describes a novel potassium channel protein (1) Kv6.2. This protein forms, with the protein Kv2.1, voltage-dependent potassium channels that are expressed preferentially in the myocardium and hippocampus and have high affinity for propafenone. The channels are used to identify specific modulators which are potentially useful as therapeutic agents, particularly as class IC anti-arrhythmics, but more generally agents for treating cardiovascular or nervous system diseases, e.g. antihypertensives or cardioprotectants, or for treating learning and memory disorders or neurodegenerative disorders such as epilepsy, ischemia, stroke, or Parkinson's or Alzheimer's diseases. Nucleic acid that encodes (1) is used for recombinant production of (1), particularly to generate cells for drug screening. (1) is also used to raise specific antibodies. This sequence encodes a fragment of the human Kv6.2 protein
                                                                                                                                                                                                                                                                 propafenone; voltage-dependent potassium channel; therapy; treatment; class IC anti-arrhythmic; cardiovascular disease; nervous system disease; antihypertensive; cardioprotectant; learning disorder; memory disorder; neurodegenerative disorder; epilepsy; ischemia; Parkinson's disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                 Kv6.2; potassium channel protein; Kv2.1; myocardium; hippocampus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New potassium channel protein, Kv6.2, used to screen for specific modulators, potentially useful e.g. as antiarrhythmic agents.
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Pred. No. 1.2e+03;
0; Mismatches 1; Indels
                                                                                                                                                                                                         Human Kv6.2 DNA containing an intron/exon boundary.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 22 BP; 4 A; 4 C; 13 G; 1 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      which corresponds to an intron/exon boundary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (GENI-) FORSCHUNGSGESELLSCHAFT GENION MBH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Page 22; 42pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          850 GCCGAGGAGGAGCTGGTG 867
 20
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                                                                                              BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  98DE-01041413.
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Best Local Similarity 94.4%;
Matches 17; Conservative
 3 ececarecaertricines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADF87858 standard; DNA; 22
                                                                                              AAZ23807 standard; DNA; 22
                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                              Alzheimer's disease; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1999-519712/44.
P-PSDB; AAY50345.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Netzer R, Pongs O;
                                                                                                                                                                                                                                                                                                                                                                                                                         DE19841413-C1.
                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    06-AUG-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       06-AUG-1998;
                                                                                                                                                                          18-JAN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                              23-SEP-1999.
                                                                                                                                  AAZ23807;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 908
ADF87858/c
ID ADF8785
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Gaps ; 0

Query Match 0.4%; Score 16.4; DB 1; Length 21; Best Local Similarity 94.4%; Pred. No. 1.2e+03; Matches 17; Conservative 0; Mismatches 1; Indels

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AAQ88807 was used in combination with AAQ88808 as primers for the PCR amplification of BoPCaR I, bovine parathyroid calcium receptor, which was used to test the effectiveness of new calci-mimetics that mimics the rection of extracellular Ca ions. These calci-mimetics can be used in the treatment of a variety of diseases associated with abnormal levels of Ca in calls, blood and plasma, specifically hyperparathyroidism. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                          Compsn. contg. partly new calci-mimetic and calcilytic cpds. - for treating parathyroidism, Paget's disease etc. and for diagnosis, also new ion receptors and associated nucleic acid, antibodies and transgenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RSE; receptor protein tyrosine kinase; rPTK; diagnostic; therapy; neurodegenerative disease; Alzheimer disease; Parkinson disease; kidney disease; primer; polymerase chain reaction; PCR; ss.
                                                                                                                                                                                              Van Wagenen BC, Balandrin MF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0.4%; Score 16.4; DB 1; Length 23; 70.0%; Pred. No. 1.3e+03; Live 5; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 23 BP; 2 A; 6 C; 2 G; 6 T; 0 U; 7 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (GETH ) GENENTECH INC.
(NEWE-) NEW ENGLAND DEACONESS HOSPITAL.
                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Page 100; 283pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Scadden DT;
                                                                                                                                                                                              Hebert SC,
                                                                                                                                  (BGHM ) BRIGHAM & WOMENS HOSPITAL. (NPSP-) NPS PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 921 CITCITCCIGITCATCCIGG 940
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 crwcrrcyrgkrsamccrsg 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        93US-00157563.
                                                       93WO-US001642
                                                                                              93WO-US001642
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   94WO-US013214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAQ94426 standard; DNA; 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (revised)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 70.0
Matches 14; Conservative
                                                                                                                                                                                            Brown EM, Del Mar EG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Godowski PJ, Mark MR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human Rse rPTK primer.
                                                                                                                                                                                                                                                         WPI; 1994-293958/36.
                                                         23-FEB-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5-NOV-1994;
                                                                                              23-FEB-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO9514776-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23-NOV-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20-DEC-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25-MAR-2003
01-NOV-1995
                    01-SEP-1994.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-JUN-1995
                                                                                                                                                                                              Nemeth EF,
Fuller FH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAQ94426;
                                                                                                                                                                                                                                                                                                                                                         animals
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 910
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to a novel polynucleotide isolated and purified from a human gene having any one of 915 fully defined sequences as given in specification, or a sequence having a base substitution. The invention further relates to: an oligonucleotide containing single nucleotide ragments from any one of 1220 fully defined sequences as given in specification, a labelling probe containing the SNP containing only on a microarray equipped with the SNP containing oligo. The isolated human gene of the invention is useful for detecting the single nucleotide polymorphisms in human gene. The isolated human gene is also useful for diagnosis of disease and determination of side effect to a medical agent. The isolated human gene is also effective in detecting single nucleotide polymorphisms in a human gene. This polymocleotide sequence represents one of the PCR primers used in the single nucleotide polymorphism
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel polynucleotide useful for detecting single nucleotide polymorphisms
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BoPCaR I; bovine parathyroid calcium receptor; hyperparathyroidism; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                    human; single nucleotide polymorphism; microarray; side effect; ss;
                                                                                              Single nucleotide polymorphism detection primer, SEQ ID No 1441.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 16.4; DB 1; Length 22;
Pred. No. 1.2e+03;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BoPCaR I, bovine parathyroid calcium receptor PCR primer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 22 BP; 10 A; 8 C; 3 G; 1 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 2; SEQ ID NO 1441; 704pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BP.
                                                                                                                                                                                                                                                                                                                                                                                                                  (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAQ88807 standard; cDNA to mRNA; 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            detection method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2351
                                                                                                                                                                                                                                                                                                                                     12-FEB-2002; 2002JP-00034717
                                                                                                                                                                                                                                                                                                                                                                           12-FEB-2002; 2002JP-00034717
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 94.4%;
warches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19 crrererererererere
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2334 CGTGTGTGTGTGTGTG
                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2003-820454/77
                                                                                                                                                                                                                                                         JP2003235571-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    human gene
                                                                                                                                                                                                                      Homo sapiens.
                                                         26-FEB-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25-MAR-2003
27-APR-1995
                                                                                                                                                                                                                                                                                            26-AUG-2003
                                                                                                                                                         primer; PCR
                                                                                                                                                                                                Synthetic.
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                    ADF87858;
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WPI; 1995-206933/27.

WO9418959-A1

RESULT 909

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AAQ88807

BXSXXXXXXXXXXXX

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Gaps

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17; Conservative
                       Local Similarity
                                                                 31-AUG-1998;
                                                            24-OCT-2002
                                                                         Marks JD,
                      Query Match
                                         ABX76679
                                                      Mus sp.
                                   Matches
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Primers given in AAQ94423-26, based on conserved sequences of tyrosine kinases, were used to amplify fragments of tyrosine kinase encoding genes from cDNA prepared from human brain RNA as an initial step toward the isolation of a new TPK gene, Rse (AAQ94421). (Updated on 25-MAR-2003 to correct PN field.)
Human and murine receptor protein tyrosine kinase(s) and corresp. DNA - for stimulation of cell growth and differentiation e.g. for treatment of neuro:degenerative and kidney diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 23 BP; 8 A; 6 C; 4 G; 3 T; 0 U; 2 Other;
                                                                                                                                                                                                                 Example 1; Page 57; 119pp; English.
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ABX76679 standard; DNA; 23 (first entry) 04-APR-2003

Bb.

Mouse heavy chain variable region PCR primer VH7 back #1.

Botulinum neurotoxin type A; BoNT/A; ss; PCR; primer; mouse; scFv; antibody; botulism; antibacterial; single chain antibody; immunoglobulin.

US2002155114-A1.

98US-00144886, 31-AUG-1998; 98US-00144886

J. (MARK/) MARKS

(AMER/) AMERSDORFER P.

Amersdorfer

WPI; 2003-182618/18.

Novel antibody that specifically binds and neutralizes botulinum neurotoxin type A useful for neutralizing botulinum neurotoxin and treating botulism.

Example 1; Page 17; 31pp; English.

an epitope specifically bound by an antibody expressed by a clone such as clone \$25, C25, C39, IC6 and clone IF3, where the antibody binds to and entralises botulinum neurotoxin type A (BONT/A). Also included are a polypeptide comprising BONT/A neutralising epitope comprising an epitope which is specifically bound by the antibody, where the polypeptide is not a full-length botulinum neurotoxin H c fragment and making an anti-BONT/A antibody that neutralises BONT/A (by contacting several antibodies with an epitope specifically bound by an antibody expressed by any of the novel clones and isolating an antibody that specifically binds to the epitope). The antibody is useful for neutralising a BONT/A, by contacting botulinum neurotoxin type A with the antibody comprising VH CDR (Heavy chain variable region complementarity determining region) and with a The invention relates to an isolated antibody that specifically binds to

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second anti-BoNT/A antibody which comprises a VH CDR, where the second antibody binds to a different epitope than the first anti-BoNT/A antibody is useful in the treatment of pathologies associated with botulinum neurotoxin poisoning, for rapid detection/diagnosis of botulism and in the detection and/or quantification of BoNT/A in a biological sample obtained from an organism which is indicative of a Clostridium botulinum infection of the organism. The present sequence is a PCR primer used to amplify mouse immunoglobulin genes for isolation/expression of the single chain antibodies (scFv) of
                                                                                                                                                                                                                                                                 the invention
           8888888888888888
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Sequence 23 BP; 4 A; 2 C; 10 G; 5 T; 0 U; 2 Other;

Gaps ö Length 23; Indels Score 16.4; DB 1; Pred. No. 1.3e+03; 2; Mismatches 3; 853 GAGGAGGAGCTGGTGGAGGCTG 874 Query Match 0.4%; Best Local Similarity 77.3%; Matches 17; Conservative : ò

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1 gargrgaagcrggrggarcrg 22

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Gaps

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3; Indels

2; Mismatches

0.4%; Score 16.4; DB 1; Length 23; 77.3%; Pred. No. 1.3e+03;

ABZ83680 standard; DNA; 23 RESULT 912 ABZ83680/

BP.

14-MAY-2003 (first entry) ABZ83680;

Toxicologically relevant human PCR primer #839.

Toxicologically relevant gene; toxicological response; PCR primer; ss.

Homo sapiens. Synthetic.

WO2003016500-A2

27-FEB-2003.

6-AUG-2002; 2002WO-US026514

(PHAS-) PHASE-1 MOLECULAR TOXICOLOGY INC.

16-AUG-2001; 2001US-0313080P.

Schmeiser K; Kier LD, Dunn RT, Adkins K, Pickett GG, Neft RE, Alen P;

Determining a toxicological response to an agent, useful for screening of drugs, comprises comparing the expression profile of one or more human toxic response genes to a reference gene expression profile indicative of WPI; 2003-268322/26.

Claim 1; Page 258; 455pp; English.

coxicity

The present invention describes a method (M1) for determining a toxicological response to an agent, which comprises comparing the expression profile of one or more human toxic response genes to a reference gene expression profile indicative of toxicity, and so determining the presence of a toxic response to the agent. Also described: (1) an array comprising one or more polynucleotides selected from the genes corresponding to the partial sequences given in AB282842 to AB284764, or their fragments of at least 20 nucleotides, or homologues is and (2) determining if a gene putatively identified to be a toxic response gene plays a role on toxic response pathways by determining the expression profile of the gene after exposure of cells or a human subject to a known toxic parameceutical or industrial agent, comprising: (a) exposing cells to an agent or isolating cells from a human subject who was exposed to an agent; (b) obtaining the test gene expression profile

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The invention relates to a novel method for identifying a B cell carrying a surface immunoglobulin (Ig) molecule having a binding site for an a surface immunoglobulin (Ig) molecule having a binding site for an tiggen of interest. The method comprises contacting a sample putatively containing the B cell with the antigen of interest and with a receptor specifically binding to the Ig molecule, and assessing the presence of the detectable signal. The invention further comprises: an antibody comprising an amino acid(B) sequence(B) given in the specification, and/or are encoded by a nucleic acid sequence(B) also given in the specification, and a device for assessing the presence of a detectable signal defined above, where the device comprises a closed system for the detection laser-beam and a catcher tube, and where the B cell of interest can be collected as a single cell by means of an electrochemical device, which is triggered by an electric signal generated by the fluorescence activated cell sorter (FACS) device, where the electrochemical device
for a putatively identified toxic response gene after exposure to a known toxic pharmaceutical or industrial agent; and (c) comparing the test profile to the expression profile of a gene with a similar function or comparing the test profile to the expression profile of that gene after exposure to other known toxic compounds. The methods are useful for exposure to other known toxic compounds. The seponess on a cellular, organ or system level. The arrays comprising the human genes are useful for toxicological screening of drugs, pharmaceutical compounds and chemicals
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     B cell VH/VL region cloning half nested PCR primer, HUVHBACK5.
                                                                                                                                                                                                                                                                                                                                                                                                                       Score 16.4; DB 1; Length 23; Pred. No. 1.3e+03;
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                                                                                                                                                                                                                                                                                                                                              Sequence 23 BP; 3 A; 10 C; 4 G; 6 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           251 TGGACAAGAAGCTGCTGG 268
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                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 94.4%;
Matches 17; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2004-449579/42
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moves the nozzle of the steady catcher tube liquid stream for a programmed time over a collecting tube, microtiter plate or other container after a B cell is sorted. The method is useful for identifying a B cell carrying a surface Ig molecule having a binding site for an antigen of interest. The method is also useful for cloning of antibody variable regions from the identified B cells, which may subsequently be employed in the construction of proteins such as antibodies or its fragments or derivatives useful in therapeutic approaches. The method is useful as an alternative to phage display for the gain of antibodies or its its fragments. This polynucleotide sequence represents a primer used in the exemplification of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               B cell; surface immunoglobulin; Ig; binding site; antigen; human CD28; closed system; detection laser-beam; catcher tube; electrochemical device; fluorescence activated cell sorter; FACS;
                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                           Indels
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                                                                                                                                                                                                                                                           Sequence 23 BP; 3 A; 3 C; 10 G; 5 T; 0 U; 2 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               antibody variable region; primer; ss; human.
                                                                                                                                                                                                                                                                                                                                             2; Mismatches
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                                                                                                                                                                                                                                                                                                  Match 0.4%;
Local Similarity 77.3%;
les 17; Conservative
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Matches
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Cornea; proliferation; in vivo; hepatocyte growth factor; injury; PCR; keratinocyte growth factor; ocular surgery; epithelium; endothelium; expression; receptor; polymerase chain reaction; amplification; primer; healing; beta-actin; upstream; downstream; intron; ss.

92US-00947683.

21-SEP-1992; 21-SEP-1992;

US5589451-A. 31-DEC-1996

Synthetic.

(TEXA) UNIV TEXAS SYSTEM.

WPI; 1997-076878/07.

Wilson SE;

HGF receptor gene upstream primer binds bases 3993-4013.

(first entry)

21-MAY-1997

AAT63277;

1 TCCCGGAAGTGTATCCACCGG 21

AAT63277 standard; DNA; 21

RESULT 916

AAT63277 ID AAT6

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which is triggered by an electric signal generated by the fluorescence activated cell sorter (FACS) device, where the electrochemical device moves the nozzle of the steady catcher tube liquid stream for a programmed time over a collecting tube, microtiter plate or other container after a B cell is sorted. The method is useful for identifying a B cell carrying a surface Ig molecule having a binding site for an entigen of interest. The method is also useful for cloning of antibody variable regions from the identified B cells, which may subsequently be employed in the construction of proteins such as antibodies or its fragments or derivatives useful in therapeutic approaches. The method is useful as an alternative to phage display for the gain of antibodies or its its fragments. This polynucleotide sequence represents a primer used in the exemplification of the invention.
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                                                                                                                                                                                                                                                                                                                                  Length 23;
                                                                                                                                                                                                                                                                                                                                                                          3; Indels
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                                                                                                                                                                                                                                                                                               Sequence 23 BP; 3 A; 3 C; 11 G; 3 T; 0 U; 3 Other;
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0.4%; Score 16.4; DB 1;
Best Local Similarity 77.3%; Pred. No. 1.3e+03;
Matches 17; Conservative 2; Mismatches 3;
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                                                                                                                                                                                                                                                                                                                                                                                                              853 GAGGAGGAGCTGGTGGAGGCTG 874
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAQ27544 standard; DNA; 21 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Promoting or suppressing corneal cell proliferation - using hepatocyte growth factor or calcium ions resp., e.g. for treating corneal injury or for preserving corneal tissue prior to transplantation.
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85.7%; Pred. No. 1.2e+03;
iive 0; Mismatches 3; Indels
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Matches
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ID AAT6
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Gaps

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0.4%; Score 16.2; DB 1; Length 21; 85.7%; Pred. No. 1.2e+03; tive 0; Mismatches 3; Indels

1603 TCCCAGAAGTGCATCCACAGG 1623

Best Local Similarity 85.7 Matches 18; Conservative

Query Match

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The present sequence was used in the development of a novel method for the inhibition of corneal epithelial cell differentiation. The method comprises contacting the cells with a hepatocyte growth factor (HGF) and/or keratinocyte growth factor (KGF). When HGF and KGF are both used, the cells can be contacted with them sequentially or simultaneously. The HGF and/or KGF is in a timed release delivery system, especially comprising biodegradable polymer microcapsules. The HGF and/or KGF are administered topically. The method is used for treating dry eye,
                                                                                                                                                                                                                                                Inhibition of corneal cell differentiation - by using hepatocyte growth factor and/or keratinocyte growth factor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HSV-1; latency associated transcript; LAT; LATin;
gene transcript stabilisation; gene expression; gene therapy; PCR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0.4%; Score 16.2; DB 1; Length 21; 85.7%; Pred. No. 1.2e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 21 BP; 0 A; 7 C; 6 G; 8 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Zabolotny JM, Krummenacher CF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (WIST-) WISTAR INST ANATOMY & BIOLOGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              especially keratoconjunctivitis sicca
                                                                                                                                                                                                                                                                                                             Example 1; Col 17-18; 36pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1807 IGGICCTTIGGGGICCTGCIC 1827
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 recretrireceretere 21
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                                         95US-00400323
                                                                                  92US-00947683
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAV64914 standard; DNA; 21
                                                                                                                        (TEXA ) UNIV TEXAS SYSTEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 85.7
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HSV-1 primer Exon 2n.
                                                                                                                                                                                                          WPI; 1998-076459/07.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human herpesvirus 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1998-609982/51.
                                         09-MAR-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO9848004-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18-APR-1997;
                                                                                21-SEP-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15-MAR-1999
30-DEC-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29-0CT-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fraser NW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAV64914;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 919
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAV64914/c
셤
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This PCR primer was used to amplify reverse transcribed cDNA which encodes a protein that is associated with liver neoplastic diseases, such as cirrhosis and hepetocellular carcinoma. This cDNA was obtained by reverse transcription of mRNA extracted from liver samples obtained from liver biopsy patients. The protein is not found in normal non-neoplastic livers, and its presence can therefore be used for diagnostic purposes. Antibodies to this protein have been produced and are expected to have some use in diagnosis, by detecting the presence or absence of the protein using, e.g BLISA assays. The antibodies may also be used in the protein using and treatment of liver neoplastic diseases. The invention also includes antisense oligonucleotides, and DNA sequences encoding antisense oligonucleotides, and DNA sequences encoding antisense neoplastic diseases, by inhibiting disease development
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Inhibition, corneal epithelial cell; differentiation, treatment, hepatocyte growth factor, HGF; keratinocyte growth factor; KGF; dry eye; keratoconjunctivitis sicca; PCR primer; receptor; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New marker gene for liver neoplastic disease - used for developing products for the diagnosis and therapy of diseases such as liver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                      Liver neoplastic disease; cirrhosis; hepatocellular carcinoma; adenomatous hyperplasia; adenoma; liver; PCR; primer; ss; polymerase chain reaction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0.4%; Score 16.2; DB 1; Length 21; 85.7%; Pred. No. 1.2e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 21 BP; 0 A; 7 C; 6 G; 8 T; 0 U; 0 Other;
                   Neoplastic disease protein upstream PCR primer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cirrhosis and hepatocellular carcinoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Upstream primer for HGF receptor DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1807 TGGTCCTTTGGGGTCCTGCTC 1827
                                                                                                                                                                                                                                                                                                                                                          (CEDA-) CEDARS SINAI MEDICAL CENT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAV05489 standard; DNA; 21 BP
                                                                                                                                                                                                                                                                        96WO-US014487.
                                                                                                                                                                                                                                                                                                                                                                                                Demetriou AA, Ljubimova JY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAY-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1997-212852/19.
                                                                                                                                                                                     WO9711968-A2
                                                                                                                                                                                                                                                                        10-SEP-1996;
                                                                                                                                                                                                                                                                                                                 27-SEP-1995;
                                                                                                                                                                                                                              03-APR-1997
                                                                                                                                             Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAV05489;
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Gaps

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Indels

Increasing expression of genes having unstable RNA transcripts, particularly for gene therapy - using a construct including gene flanked by intron fragments that include a hairpin next to the intron branchpoint.

Ното варіеля

Synthetic

Matches

8 요 US5703047-A

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This sequence represents a PCR primer for DNA encoding a human antiFC epsilon RI alpha chain antibody, produced using the method of the invention. The method is for preparing an antibody Pab fragment using the yeast Pichia pastoris as the host call. The method can prepare an antibody Fab fragment cost efficiently and in high yield
                                           This is the nucleotide sequence of primer Exon 2n, which was used with primer Exon 1 (see AAV64912) in RT-PCR to characterise the splice junctions of the latency associated transcript (LAT) of herpes simplex virus type 1 (see AAV64883-86). The invention relates to methods of stabilising unstable gene transcripts. A claimed polynucleotide comprises: a polynucleotide encoding a gene product; a 5'-sequence of an intron, including the splice donor and splice acceptor sites (see AAV64885-86), and a 3'-sequence of the same intron, including a hairpin structure (see AAV64887) next to the intron's branchpoint. A preferred intron is the 2.0 kb LAT of a herpes virus. Methods and compositions
                                                                                                                                                                                                                                  using the polynucleotide can be used in gene therapy and more generally as research reagents, markers of gene production, in therapeutic or diagnostic compositions, in drug screening and to identify transcripts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AntiFc epsilon RI alpha chain antibody; antibody production; human; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Primer for antifc epsilon RI alpha chain antibody coding sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Preparing an antibody Fab fragment using yeast - in high yield
                                                                                                                                                                                                                                                                                                                                                               Query Match 0.4%; Score 16.2; DB 1; Length 21; Best Local Similarity 85.7%; Pred. No. 1.2e+03; Matches 18; Conservative 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                         produced only at selected stages of the cell cycle
                                                                                                                                                                                                                                                                                                                             Sequence 21 BP; 0 A; 11 C; 2 G; 8 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 21 BP; 3 A; 3 C; 10 G; 5 T; 0 U; 0 Other;
                 Example 1; Page 23; 106pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                          183 CGGGGAGGACGAGGCTGAGGA 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 2; Page 4; 13pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21 CGAGGAGGAAGAGGCAGAGGA 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAX01222 standard; DNA; 21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TORII YAKUHIN KK.
NIKKA WHISKEY KK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1999-124394/11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (ASAK ) ASAHI
(TORI ) TORII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              JP11000174-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13-JUN-1997;
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0.4%; Score 16.2; DB 1; Length 21;

Query Match

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    malignancy-associated gene (MAG) proteins. The polypeptide is useful for detecting antibodies associated with liver disease. Probes derived from the MAG gene are useful for detecting the presence of sequences associated with neoplastic disease, e.g. liver diseases such as cirrhosis and hepatocellular carcinoma, and therefore can be used in disease and hepatocellular carcinoma, the development of therapeutics that are useful for inhibition of the development of neoplastic liver disease. PCR primers AAX81822-23 were used in the course of the invention
                                                                                                                                                                                                                                                                               Liver neoplastic disease, malignancy-associated gene; MAG; liver disease; neoplastic disease; cirrhosis; hepatocellular carcinoma; FCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         specification describes a liver neoplastic disease polynucleotide and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Liver-associated malignancy-associated gene (MAG), useful for screening for cirrhosis and hepatocellular carcinoma.
                                                                                                                                                                                                                                                    PCR primer used to amplify cDNA sequences isolated from liver tissue.
                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                             Indels
85.7%; Pred. No. 1.2e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 21 BP; 0 A; 7 C; 6 G; 8 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mouse insulin PCR primer Insl3 SEQ ID NO:4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ljubimova JY, Demetriou AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1807 TGGTCCTTTGGGGTCCTGCTC 1827
                                                          873
                                                                                      1 gaggrecagérégrégagrer 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (CEDA-) CEDARS SINAI MEDICAL CENT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 3; Page 13; 42pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 TGGTCCTTTGGCGTCGTCCTC
                                                          853 GAGGAGGAGCTGGTGGAGGCT
                                                                                                                                                                BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  97US-00989750
                                                                                                                                                                AAX81822 standard; DNA; 21
                                                                                                                                                                                                                         (first entry)
                             18; Conservative
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                Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                     11-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                            WO9929859-A1
                                                                                                                                                                                                                         02-SEP-1999
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                                                                                                                                                                                                                                                                                                                              Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Black K,
                                                                                                                                                                                             AAX81822;
                                                                                                                                    RESULT 921
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                              Matches
                                                                                                                                                   AAX81822
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The present invention describes the a method for screening potential inhibitors of the expression of the Pax4 gene by contacting the potential inhibitor with parcreatic beta cells and measuring the expression of the gene in these cells is new. Substances identified by the screening method potentiate the expression of the Pax4 gene in pancreatic beta cells and accelerate the expression of insulin gene in those cells. The method can be used in the treatment of disorders in which the exhaustion of pancreatic beta cells is involved, such as diabetes. The present sequence represents a PCR primer which is used in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 antiinflamatory; antiulcer; cytostatic; antipsoriatic; antiparkinsonian; noutoropic; neuroprotective; vasotropic; chemotaxic; angiogenic; neuroprotective; vasotropic; chemotaxic; angiogenic; antiarthritic; antiarthritic; antiarthritic; antirhumatic; antiarthritic; antiarthritic; antirhumatic; thrombolytic; immunomodulator; enterocolitis; Collinger-Ellison syndrome; gastrointestinal ulceration; psoriasis; cancer; Parkinson's disease; Alzhaimer's; ALS, neuropathy; dermal scarring; wound healing; nerve repair; thrombosis; bone; cartilage formation; angiogenesis; atherostoid arthritis; multiple scalerosis; inflammatory disorder; atherosclerosis; cardiac injury; infertility; premature aging; AlDS; diabetes; stroke; gene therapy; transgenic; PRO; human; ss; primer; PCR.
                                                                                                                                                                                                                                                                                                                                Screening potential Pax4 gene potentiators, used in treatment of, e.g.
diabetes.
Human; activin A; Pax4 gene; expression; potentiator; insulin;
pancreatic beta cell; diabetes; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0.4%; Score 16.2; DB 1; Length 21; ilarity 85.7%; Pred. No. 1.2e+03; Conservative 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human PRO protein-related reverse PCR primer SEQ ID 312.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 21 BP; 2 A; 6 C; 7 G; 6 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Page 17; 38pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GAAGTGCATCCACAGGGACCT 1628
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21 GAAGCGCATCCACAGGGCCAT 1
                                                                                                                                                                                                                                       (YAMA ) YAMANOUCHI PHARM CO LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BP
                                                                                                                                                                  99WO-JP003182.
                                                                                                                                                                                                    98JP-00167976.
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                                                                                                                                                                                                                                                                                                               WPI; 2000-097752/08
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              present invention
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                                                                                       WO9966073-A1
                                                                                                                                                              15-JUN-1999;
                                                                                                                                                                                                    16-JUN-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-JAN-2004
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                                                                                                                            23-DEC-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADC78624;
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                                                                                                                                                                                                                                                                           Ueda Y;
                                                       Mus sp
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Matches
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Gaps

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The polypeptides and polyucclectides of the invention may be useful as research tools and as therapeutics for treating enterocolitis, Zollinger-Bilson syndrome, gastrointestinal ulceration, psoriasis, cancer, Parkinson's disease, Alzheimer's disease, ALS, neuropathies, dermal scarring and wound healing, nerve repair, thromboals, bone and/or cartilage formation, angiogenesis, asthma, rheumatoid arthritis, multiple sclerosis, inflammatory disorders, atherosclerosis, cardiac injury, infertility, premature aging, AIDS, diabetes complications and stroke. The molecules may also be utilised during gene therapy procedures and transgenic animal production. The current sequence is that of the PCR primer of the invention which was used to analyse the human PRO DNA of
                                                                                                                                                                                                Novel nucleic acids encoding secreted and transmembrane polypeptides with homology, e.g. to growth and cancer-associated antigens.
                                                                                                                                                                                                                                                                                    The invention relates to a novel nucleic acid encoding a PRO polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Determining genetic risk of arteriosclerosis, for clinical diagnosis, comprises hybridizing patient nucleic acid with an array of probes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Arteriosclerosis; diagnosis; hybridisation; synergism; gene therapy;
                                                                                                                Hillan K, Pennica D, Wood WI;
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0.4%; Score 16.2; DB 1; Length 21;
Best Local Similarity 85.7%; Pred. No. 1.2e+03;
Matches 18; Conservative 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 21 BP; 4 A; 5 C; 8 G; 4 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Arteriosclerosis-detecting probe from HNF1 #4.
                                                                                                                                                                                                                                               Example 44; SEQ ID NO 312; 355pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1254 CATTGACAAGGACCGGCCGC 1274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21 CATTTCCAAGGACCTGGCCGC 1
                                                                                                                Goddard A, Gurney AL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BP.
                 99WO-US021090
                                                98WO-US019330
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13-MAR-2001; 2001DE-01011925
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABX09458 standard; DNA; 21
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                                                                               (GETH ) GENENTECH INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Seedorf U;
                                                                                                                                                                 WPI; 2000-271434/23.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              mutation; probe; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (OGHA-) OGHAM GMBH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200272882-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the invention.
                 15-SEP-1999;
                                                16-SEP-1998;
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                                                                                                                Chen J,
Yuan J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABX09458;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 924
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mutations; (ii) applying probes from these sequences, or their complements, to a carrier; (iii) hybridising the probes with a mucleic acid from (or synthesised from) a patient sample; and (iv) detecting and evaluating the hybridisation pattern. The method provides a quick, inexpensive and informative diagnosis, and makes possible a multifactorial analysis for detecting e.g. synergism between different mutations or mutations that when present alone carry no risk but are risk associated in presence of other mutations. The results may be combined with known risk sasessement methods to provide a more reliable diagnosis, especially important with new therapeutic methods (e.g. gene therapy) that are directed against specific genes. All relevant mutations in a reference can be screened for in a single test and the method is well suited to automation. ABX09147-ABX09676 represent probes used to illustrate the method of the invention
                                                                                                        This invention describes a novel method for determining the genetic risk of arteriosclerosis both for clinical diagnosis and for population studies. The method comprises: (1) selecting risk-associated reference nucleic acid sequences, including their functionally characterizing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
derived from risk-associated reference genes and their mutations
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 21 BP; 2 A; 13 C; 6 G; 0 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2907 CAGGCATGGCCCTGGGCGGGG 2927
                                                     Example 1; Page 126; 146pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           85.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity 85.7
Les 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
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8
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21 ceseccreeccreeceses 1 g

ACA60810 standard; DNA; 21 BP. 01-JUL-2003 (first entry) ACA60810; RESULT 925 ACA60810

Hamster anti-CD3 epsilon antibody 145-2C11 PCR primer number 7.

Antibody; PD-1; J43; immunopathy; neurodegenerative disease; Parkinson's disease; Parkinson's syndrome; Huntington's disease; Machado-Joseph disease; amyotrophic lateral sclerosis; SS; PCR; primer; Creutzfeldt-Jakob disease; autoimmune disease; glomerulomephritis; arthritis; myocardiopathy-like disease; ulcerative colitis; Sjogren's syndrome; Crohn's disease; systemic erythematosus; multiple myosititis; skin toughening; rheumatic fever; CD3; 145-2C11; insulin-dependent diabetes; Behoet's disease; Hashimoto disease; periarteritis nodosa; leukoderm vulgaris; Armenian hamster.

Cricetulus migratorius

WO2003011911-A1

13-FEB-2003.

30-JUL-2002; 2002WO-JP007735.

31-JUL-2001; 2001JP-00232303

(ONOY) ONO PHARM CO LID. (HONJ/) HONJO I.

Matsuo M, Honjo T, Shibayama S,

Yoshida T;

WPI; 2003-248150/24

Substance specific to PD-1, selectively recognizing PD-1 and a related cell membrane protein, applicable in developing remedies or preventives

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The invention relates to a substance comprising a substance recognising

CD The call membrane where PD-1 is expressed, and a linker. Also included is

CD the cell membrane where PD-1 is expressed, and a linker. Also included is

CD a drug composition containing an effective dose of a remedy and/or

CD preventive for PD-1 related disease namely immunopathy, e.g.

CD preventive for PD-1 related disease namely immunopathy, e.g.

CD preventive for PD-1 related disease, manchy immunopathy, e.g.

CD preventive for PD-1 related disease, manchy immunopathy, e.g.

CD preventive for PD-1 related disease, manchy immunopathy, e.g.

CD preventive for PD-1 related disease, manchadon-Oseph disease, anyotrophic

CD lateral sclerosis, and Creutzfeldt-Jakob disease, and autoimmune

CD diseases, e.g. glomerulorephritis, arthritis, mycardiopathy-like

CD diseases, ulcerative colitis, Sjogren's syndrome, Crohn's disease,

CD systemic erythematosus, multiple myosititis, skin toughening, rheumatic

CD erver, insulin-dependent diabetes, Behcet's disease,

CD eriarteritis nodosa, and leukoderm vulgaris. A chimaeric protein of the

CD entito was created comprising the light and heavy chains of the mouse

CD existent the hamster 145-2C11. The present sequence is a PCR primer used to

CD amplify the hamster 145-2C11 cDNA sequence
for diseases caused by immunopathy e.g. autoimmune diseases
                                                               Example 7; Page 32; 73pp; Japanese.
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Gaps .; 0 0.4%; Score 16.2; DB 1; Length 21; 85.7%; Pred. No. 1.2e+03; tive 0; Mismatches 3; Indels 853 GAGGAGGAGCTGGTGGAGGCT 873 21 1 GAGGIGCAGCIGGIGGAGICI Best Local Similarity 85.7 Matches 18; Conservative Query Match à 원

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Sequence 21 BP; 3 A; 3 C; 10 G; 5 T; 0 U; 0 Other;

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ADI00328 standard; DNA; 21 BP

ADI00328;

22-APR-2004 (first entry)

PCR primer SEQ ID 108 used to amplify human PKD-1 exon 15L DNA.

mutation analysis; PKD; polycystic kidney disease; human; PKD-1; ss; PCR;

Homo sapiens.

US2003152936-A1.

14-AUG-2003.

26-FEB-2002; 2002US-00083246..

12-OCT-2001; 2001US-0328739P.

(ATHE-) ATHENA DIAGNOSTICS INC.

<u>ن</u> Wang Robichaud NJ, Allen SK, , Curran JA, Palatucci CM; Hennigan AN, Garces JA, Jones JG, Flynn KE,

WPI; 2003-897708/82.

Analyzing mutations of a target nucleic acid by detecting heteroduplexes from generated duplexes, useful for diagnosing patients affected with polycystic kidney disease.

Disclosure; SEQ ID NO 108; 126pp; English.

one first The invention relates to a novel method of mutation analysis of a target nucleic acid which comprises incubating a sample having the target nucleic acid in a reaction mixture, in the presence of at least one first and second nucleic acid, where incubation produces amplified products, vivlemore401-10.rng

Human Flt-1 DNA sequence, a target for siRNA inhibition SeqID 415

(first entry)

06-MAY-2004

ADJ97642;

ADJ97642 standard; DNA; 21 BP.

RESULT 92 ADJ97642

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generating duplexes in the amplified products and detecting the presence or absence of a heteroduplex from the duplexes, where its presence indicates a potential mutation in the target nucleic acid and its absence indicates the absence of mutation in the target nucleic acid. The method and compositions of the invention may be useful for analysing mutation. The current sequence is that of a PCR primer of the invention which RD (polycystic kidney disease). The current sequence is that of a PCR primer of the invention which was used to amplify human polycystic kidney disease PKD-1 DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Detecting Ig-unmutated chronic lymphocytic leukemia in a subject involves determining over expression of ZAP-70 molecule in a subject.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention relates to a method of detecting Ig-unmutated chronic lymphocytic leukaemia (CLL)/small lymphocytic lymphoma (SLL) in subject. The method involves determining whether the subject overexpresses ZAP-70, which is used a marker for CLL/SLL. Also disclosed is a kit for detecting overexpression of ZAP-70 in a subject, preferably human. The present sequence represents a PCR primer used in
                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ig-unmutated; chronic lymphocytic leukaemia; CLL;
small lymphocytic lymphoma; SLL; ZAP-70; cytostatic; human; Ig VH;
framework region 1; FR1; PCR; primer; ss.
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                                                                                                                                                                                                               0.4%; Score 16.2; DB 1; Length 21; 85.7%; Pred. No. 1.2e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Wiestner A;
                                                                                                                                                                                                                                                    3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PCR primer for human Ig VH3 DNA framework region 1 (FR1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 21 BP; 3 A; 3 C; 10 G; 5 T; 0 U; 0 Other;
                                                                                                                                                                          Sequence 21 BP; 4 A; 5 C; 9 G; 3 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                    0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the examples of the present invention.
                                                                                                                                                                                                                                                                                         2239 CACCCTGCTGCTGCTACAG 2259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 2; Page 13; 32pp; English.
                                                                                                                                                                                                                                                                                                                            21 caccrrecrecrescocacae 1
                                                                                                                                                                                                                                                                                                                                                                                                                       ADH47876 standard; DNA; 21 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25-APR-2002; 2002US-0375966P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               03-DEC-2002; 2002US-00309548.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25-MAR-2004 (first entry)
                                                                                                                                                                                                  Query Match
Best Local Similarity 85.79
...-hes 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rosenwald A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2004-141578/14.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Staudt LM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADH47876;
                                                                                                                                                                                                                                                                                                                                                                                  RESULT 927
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This invention relates to novel compositions that comprise short interfering RNA (siRNA) molecules, which can be used to inhibit angionesis. Specifically, it refers to siRNAs that target and cause RNAi-induced degradation of mRNA from human vascular endothelial growth factor (VEGF), the VEGF receptor (Flt-1) and the Flk-1/KDR (kinase domain region) genes, as well as mutants derived thereof. The present invention describes sense and antiense RNA strands that form an RNA duplex and bind to the target mRNA, such that expression is inhibited and the target degraded. As such, siRNA administered in combination with a therapeutic agent is useful for treating diseases associated with angiogenesis and the overexpression of VEGF, which include diabetic retinopathy, agerelated macular degeneration, inflammatory disease, psoriasis and related macular degeneration, inflammatory disease, psoriasis and cancers including breast, retinoblatoms, Wilm's tumour and lymphoma. Accordingly, these compositions exhibit cytostatic, and indiabetic, and arthritis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel short interfering RNA (siRNA) comprises sense and antisense RNA strands, useful for inhibiting expression of human vascular endothelial growth factor mRNA, for treating angiogenic disease, e.g. diabetic
                                                                                                                                          human; ss; short interfering RNA; siRNA; angiogenesis; vascular endothelial growth factor; VEGF; VEGF receptor; Flt-1; Flk-1/KDR; kinase domain region; diabetic retinopathy; age-related macular degeneration; inflammatory disease; psoriasis; rheumatoid arthritis; cancer; breast; retinobiastoma; Wilm's tumour; lymphoma; cytostatic; antidiabetic; ophthalmological; antinflammatory;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ophthalmological, antiinflammatory, antipsoriatic, antirheumatic and antiarthritic activities. This oligonuclectide is a human Flt-1 DNA oligo, a target for siRNA inhibition of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 21 BP; 5 A; 5 C; 6 G; 5 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                      antipsoriatic; antirheumatic; antiarthritic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; SEQ ID NO 415; 218pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1609 AAGTGCATCCACAGGGACCTG 1629
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                                                                                                                                                                                                                                                                                                                                                                                                                                               18-JUL-2003; 2003WO-US022444.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24-JUL-2002; 2002US-0398417P.
14-NOV-2002; 2002US-00294228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity 85.7%;
Les 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (UYPE-) UNIV PENNSYLVANIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Reich SJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                retinopathy and cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2004-203472/19.
                                                                                                                                                                                                                                                                                                                                                            WO2004009769-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tolentino MJ,
                                                                                                                                                                                                                                                                                                                    Homo sapiens.
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Gaps

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0.4%; Score 16.2; DB 1; Length 21; 1larity 85.7%; Pred. No. 1.2e+03; Conservative 0; Mismatches 3; Indels

Local Similarity es 18; Conserv

Query Match Best Loca Matches 854 AGGAGGAGCTGGTGGAGGCTG 874 Accrecaciócrecación 21

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predictor set; protein tyrosine kinase biomarker; cytostatic; antiangiogenic; vasotropic; vulnerary; pharmacogenomic; drug sensitivity; breast cancer; hypervascular disease; angiogenesis; wound healing scar; human; ss; antisense; RNA; interfering RNA; DNA-RNA hybrid; ephA2-4.

/*tag= a /note= "Deoxyribonucleotide (thymine)"

Location/Qualifiers 20. .21

Antisense RNAi DNA-RNA hybrid oligo 2 targeted to human ephA2-4.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel short interfering RNA (siRNA) comprises sense and antisense RNA strands, useful for inhibiting expression of human vascular endothelial growth factor mRNA, for treating angiogenic disease, e.g. diabetic
                                                                                                                                                                                                                                                                                                                                                                                                            human; 88; short interfering RNA; siRNA; angiogenesis; vascular endothelial growth factor; VEGF, VEGF receptor; Flt-1; Flk-1/KDR; kinase domain region; diabetic retinopathy; age-related macular degeneration; inflammatory disease; psoriasis; rheumatoid arthritis; cancer; breast; retinoblastoma; Wilm's tumour; lymphoma; cytostatic; antidiabetic; ophthalmological; antiinflammatory; antipsoriatic; antirheumatic; antiathritic.
                                                                                                                                                                                                                                                                                                                                    Human Flt-1 DNA sequence, a target for siRNA inhibition SeqID 413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0.4%; Score 16.2; DB 1; Length 21; 55.7%; Pred. No. 1.2e+03; ve 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 21 BP; 6 A; 3 C; 9 G; 3 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; SEQ ID NO 413; 218pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18-JUL-2003; 2003WO-US022444.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24-JUL-2002; 2002US-0398417P.
14-NOV-2002; 2002US-00294228.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 85.7%;
Matches 18; Conservative
                                                                                    ADJ97640 standard; DNA; 21
                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (UYPE-) UNIV PENNSYLVANIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Folentino MJ, Reich SJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   retinopathy and cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2004-203472/19.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                29-JAN-2004.
                                                                                                                                                                                                                                                         06-MAY-2004
                                                                                                                                                                             ADJ97640;
RESULT 929
                                                ADJ97640
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to a novel predictor set comprising a plurality of polynucleotides and/or polypeptides whose expression pattern is predictive of the response of cells to treatment with a compound that modulates protein tyrosine kinase activity or members of the protein tyrosine kinase pathway. The molecules of the invention demonstrate cytostatic, antiangiogenic, vasotropic and vulnerary activities and may be useful in the field of pharmacogenomics, in particular for determining drug sensitivity and in treating breast cancer, hypervascular diseases, angiogenesis and scars in wound healing. The current sequence is that of an antisense RNAi (interfering RNA) DNA-RNA hybrid oligonucleotide which was targeted to a human protein tyrosine kinase biomarker polynucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New predictor sets with a plurality of polynucleotides and/or polypeptides whose expression pattern predicts cell response to a compound that modulates protein tyrosine kinase activity, useful in
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85.7%; Pred. No. 1.2e+03;
tive 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 21 BP; 4 A; 4 C; 7 G; 2 T; 4 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 5; SEQ ID NO 557; 649pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          448 AACTACACCTGCGTCGTGGAG 468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21 AACTACACCTTCACCGTGGAG 1
(BRIM ) BRISTOL-MYERS SQUIBB CO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hb.
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Best Local Similarity 85.7
Matches 18; Conservative
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Gaps

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RESULT 930

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Detecting polymorphisms between 2 nucleic acid samples, esp. in microsatellite regions, comprises digesting the nucleic acid to generate fragments, ligating adaptor segments to their ends, amplifying them using primer directed amplification and comparing the prode to detect differences. The primers used in the amplification comprise a primer consisting of a perfect cpd. simple sequence repeat (SSR), and an adaptor directed primer, comprising a sequence complementary to an adaptor segment. The present sequence is an example of a compound SSR primer method represents a modified amplified fragment length polymorphism and partic, useful for genome fingerprinting, i.e. for
                                                                                                                                                                                                                                   Modified amplified fragment length polymorphism assay - for detection of polymorphism esp. in micro:satellite regions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 16.2; DB 1; Length 22; Pred. No. 1.3e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 22 BP; 8 A; 0 C; 3 G; 11 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           genetic trait marking and germplasm comparisons
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                       DUPO ) DU PONT DE NEMOURS & CO E I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2823 TATATATACATATATATAT 2843
                                                                                                                                                                                                                                                                                                 Disclosure, Fig 1c, 173pp, English.
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                          95WO-US015150
                                                                94US-00346456
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Best Local Similarity 85.7%;
Matches 18; Conservative
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ID AAT30422 standard; DNA; 22
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                                                                                                                                                    Morgante M, Vogel JM;
                                                                                                                                                                                         WPI; 1996-277795/28.
                        21-NOV-1995;
                                                                28-NOV-1994;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAT30422;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Detecting polymorphisms between 2 nucleic acid samples, esp. in microsatellite regions, comprises digesting the nucleic acid to generate fragments, ligating adaptor segments to their ends, amplifying them using primer directed amplification and comparing the prods. to detect differences. The primers used in the amplification comprise a primer consisting of a perfect cpd. simple sequence repeat (SSR), and an adaptor segment. The present sequence is an example of a compound SSR primer. The method represents a modified amplified fragment length polymorphism assay, which is partic. useful for genome fingerprinting, i.e. for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Modified amplified fragment length polymorphism assay - for detection of polymorphism esp. in micro:satellite regions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                 Detection; polymorphism; perfect compound simple sequence repeat; adaptor directed primer; genome; genetic; fingerprinting; amplified fragment length polymorphism assay; microsatellite region; genetic trait marking; germplasm comparisons; compound; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Detection; polymorphism; perfect compound simple sequence repeat; adaptor directed primer; genome; genetic; fingerprinting, amplified fragment length polymorphism assay; microsatellite region; genetic trait marking; germplasm comparisons; compound; ss.
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                                          Compound simple sequence repeat primer (AT) 6.5 (GT) 4.5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Compound simple sequence repeat primer (AT)8.5(GT)3.5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 22 BP; 6 A; 0 C; 5 G; 11 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             genetic trait marking and germplasm comparisons
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Fig 1c; 173pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21 ACACACATATATATATATA 1
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                                                                                                                                                                                                                                                                                                                                                               94US-00346456
(first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Morgante M, Vogel JM;
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28-JAN-1997
                                                                                                                                                                                                                                 WO9617082-A2
                                                                                                                                                                                                                                                                                                                   21-NOV-1995;
                                                                                                                                                                                                                                                                                                                                                               28-NOV-1994;
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                                                                                                                                                                                         Synthetic
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Gaps

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Indels

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Modified amplified fragment length polymorphism assay - for detection of polymorphism esp. in micro:satellite regions.
                                                                                         Detection; polymorphism; perfect compound simple sequence repeat; adaptor directed primer; genome; genetic; fingarprinting, amplified fragment length polymorphism assay; microsatellite region; genetic trait marking; germplasm comparisons; compound; ss.
Compound simple sequence repeat primer (AT)8.5(GT)3.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (DUPO ) DU PONT DE NEMOURS & CO E I.
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WO9617082-A2

Synthetic

RESULT 932

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Sequence 22 BP; 6 A; 0 C; 5 G; 11 T; 0 U; 0 Other;

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Detecting polymorphisms between 2 nucleic acid samples, esp. in microsatellite regions, comprises digesting the nucleic acid to generate fragments, ligating adaptor segments to their ends, amplifying them using primer directed amplification and comparing the prods. to detect differences. The primers used in the amplification comprise a primer directed sprimer, comprising of a perfect cpd. simple sequence repeat (SSR), and an adaptor segment. The present sequence is an example of a compound SSR primer. The method represents a modified amplified fragment length polymorphism assay, which is partic, useful for genome fingerprinting, i.e. for genetic trait marking and germplasm comparisons
                                                    Detecting polymorphisms between 2 nucleic acid samples, esp. in microsatellite regions, comprises digesting the nucleic acid to generate fragments, ligating adaptor segments to their ends, amplifying them using primer directed amplification and comparing the prods. to detect differences. The primers used in the amplification comprise a primer consisting of a perfect cpd. simple sequence repeat (SSR), and an adaptor edgment. The present sequence is an example of a compound SSR primer repeated primer sequence is an example of a compound SSR primer method represents a modified amplified fragment length polymorphism assay, which is partic, useful for genome fingerprinting, i.e. for
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Detection; polymorphism; perfect compound simple sequence repeat; adaptor directed primer; genome; genetic; fingerprinting; amplified fragment length polymorphism assay; microsatellite region; genetic trait marking; germplasm comparisons; compound; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0.4%; Score 16.2; DB 1; Length 22; 35.7%; Pred. No. 1.3e+03; Ive 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Compound simple sequence repeat primer (AT)6.5(GT)4.5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 22 BP; 8 A; 0 C; 3 G; 11 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                genetic trait marking and germplasm comparisons
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Disclosure; Fig 1c; 173pp; English
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nes 18; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1996-277795/28.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO9617082-A2
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Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 93.0407/10 AAT30407/10 
8 X C C C C C C C C C X X X
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Gaps

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This sequence represents an oligonucleotide used in the construction of gag-pol expression cassettes. The invention relates to a retroviral vector construct which consists of a 5'-long terminal repeat (5'-LTR); a tRNA binding site; an origin of second strand DNA synthesis, a 3'-LTR and gag/pol sequences modified to contain two or more stop codons. The invention also relates to a gag/pol expression cassette, and an envexpression cassette. The retroviral construct has anticaner, antiviral and immunomodulatory activity. The retroviral constructs are used to produce recombinant retroviral particles for use in gene transfer, particularly gene therapy, e.g. to deliver heterologous sequences that encode cytotoxins, produng activators, replacement genes, antisense
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     encode cytotoxins, prodrug activators, replacement genes, antisense sequences or ribozymes, immune accessory molecules and viral immunogens, particularly for treatment or prevention of tumours, viral infections and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New retroviral construct, used to produce retroviral particles for gene therapy, containing a gag/pol sequence that includes at least two stop codons, incapable of producing replicable virus by recombination.
                                                                                                                                                                                                                                                                                                                                              Gag; pol; retroviral vector construct; gag/pol expression cassette; anticancer; antiviral; immunomodulatory; cytotoxin; prodrug activator; replacement gene; antisense sequence; ribozyme; tumour prevention; viral infection; genetic disorder; ss.
                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                Oligonucleotide #1 used in gag-pol expression cassette construction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Respess JG;
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
0.4%; Score 16.2; DB 1; Length 22; 85.7%; Pred. No. 1.3e+03; Live 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 0.4%; Score 16.2; DB 1; Length 22; Best Local Similarity 85.7%; Pred. No. 1.3e+03; Matches 18; Conservative 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Driver DA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 22 BP; 9 A; 3 C; 2 G; 8 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bodner M,
                                                                          2824 ATATATATATATATA 2844
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 3; Col 24; 63pp; English.
                                                                                               21 ACACACATATATATATA 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sauter S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           95US-00437465.
96US-00643411.
96US-00721327.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         97US-00850961.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            94US-00240030.
                                                                                                                                                                                                       AAZ90067 standard; DNA; 22
                                                                                                                                                                                                                                                                             (first entry)
   Query Match 0.4
Best Local Similarity 85.7
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Depolo NJ, Chada S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (CHIR ) CHIRON CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2000-159877/14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              genetic disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            09-MAY-1994;
09-MAY-1995;
06-MAY-1996;
                                                                                                                                                                                                                                                                             09-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         05-MAY-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26-SEP-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US6013517-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11-JAN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Synthetic.
                                                                                                                                                                                                                                           AAZ90067;
                                                                                                                                                                       RESULT 935
                                                                                                                                                                                          AAZ90067,
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2819 ATGGTATATATACATATAT 2839

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The invention relates to a gag/pol expression cassette comprising a promoter, a gag/pol gene (I) and a polyadenylation sequence in which the 5' end of (I) has been modified to contain codons that are degenerate for gag, or the 3' end of (I) has been deleted without affecting the biological activity of the encoded integrase. The expression cassette and similar cassettes that express env protein, are used to produce recombinant retrovital particles by homologous recombination. These particles are gene transfer vectors, particularly for gene therapy of tumours or viral infections, also to induce an immune response, to treat or prevent diseases, or to suppress graft rejection or immune/autoimmune responses. This sequence represents an oligonucleotide primer used in construction of gag/pol expression cassettes of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New gag/pol expression cassette, for preparing retroviral particles for gene therapy, comprises a promoter, a gag/pol gene, and a polyadenylation sequence, and cannot form a replication competent virus by homologous recombination.
                                                                                          gag/pol expression cassette; gag; pol; env; integrase; gene therapy; ss; tumour; cancer; viral infection; immune response; autoimmune response; graft rejection; cytostatic; antiviral; immunostimulant; PCR; primer; immunosuppressive; murine leukaemia virus 4070A amphotropic envelope; bovine growth hormone polyadenylation sequence; long terminal repeat.
                                                                      murine leukaemia virus; mouse; retroviral backbone; LTR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0.4%; Score 16.2; DB 1; Length 22; 85.7%; Pred. No. 1.3e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              human; collagenous matrix; hydroxyallysine cross-link;
                              Gag/pol expression cassette construction primer #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 22 BP; 9 A; 3 C; 2 G; 8 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sauter S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2819 ATGGTATATATATATAT 2839
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chada S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 3; Col 24; 63pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21 Argerarcararararar 1
                                                                                                                                                                                                                                                                                                                                                                                                             94US-00240030.
95US-00437465.
96US-00643411.
96US-00721327.
97US-00850961.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADH69177 standard; DNA; 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Depolo NJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PLOD2 PCR primer #15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (CHIR ) CHIRON CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2002-163181/21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                    MOMLV; Moloney
                                                                                                                                                                                                                                                                                      US6333195-B1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       кевревв ЈG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                         06-MAY-1996;
26-SEP-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      05-MAY-1997;
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                                                                                                                                                                                                                                                                                                                              25-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                      09-MAY-1995
                                                                                                                                                                                                                                            Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADH69177;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADH69177,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention describes a method for detecting the presence of polymorphisms associated with inflammatory bowel diseases such as ulcerative colitis and Crohn's disease. The methods can be used to detect the presence of genetic polymorphisms associated with inflammatory bowel disease and correlating their occurrence with disease states. They may be used in this way for phenotypic correlations, forensics, paternity testing, medicine and genetic analysis. The present sequence is a polymorphic site described in the exemplification of the invention
                                                                                                                                                                                                                                                                                                   Human; inflammatory bowel disease; Crohn's disease; ulcerative colitis; single nuclectide polymorphism; SNP; chromosome 19p13; paternity test; chromosome 5q31-33; forensic test; gene therapy; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Testing for the presence of polymorphisms associated with inflammatory bowel disease, using a hybridization assay.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                           Human inflammatory bowel disease associated polymorphic site #754
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /*tag= a
/note= "SNP, optionally T or A at this position"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0.4%; Score 16.2; DB 1; Length 22; 31.8%; Pred. No. 1.3e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lander ES, Rioux J, Siminovitch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Seguence 22 BP; 11 A; 3 C; 0 G; 7 T; 0 U; 1 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (WHED ) WHITEHEAD INST BIOMEDICAL RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (ELLI-) ELLIPSIS BIOTHERAPEUTICS CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3469 TATCTATATATATATTATTG 3490
                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22 TATATATATATATANGTTGTTG 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; Page 71; 463pp; English.
21 ATGGTATCGATATATATAT
                                                                                                                                  AAH91679 standard; DNA; 22 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABK33880 standard; DNA; 22 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11-DEC-2000; 2000WO-US033632.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10-DEC-1999; 99US-0170257P
10-APR-2000; 2000US-0196046P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        81.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hudson IJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2001-367874/38.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200142511-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                   Key
misc_feature
                                                                                                                                                                                                                    09-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14-JUN-2001
                                                                                                                                                                            AAH91679;
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                                                                                   RESULT 936
AAH91679/c
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Gaps

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Indela

Matches

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ABK33880/c
ID ABK33
XX
AC ABK33
XX

cross-link; proteolytic degradation; fibrosis;

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comprises cross-linked collagen molecules, where the resistance of the collagenous matrix against proteolytic degradation is controlled by controlling the ratio of hydroxyallysine cross-links to allysine cross-links comprising cross-linked collagen molecules, where the resistance of the collagenous matrix. The method is useful for by the collagen molecules, where the method is useful for treating a fibrotic condition in a mammal by administering to the mammal (preferably human) an effective amount of a composition which reduces the lysyl hydroxylation level of collagen telopeptides and thereby results in a collagenous matrix having a decreased ratio of hydroxyallysine cross-links. The method comprises administration of compound or composition that inhibits the activity or production of TLM encoded by a proble gene but not the activity or production of lysyl oxidase. The method is useful for treating fibrosis by inhibiting fibrotic processes, in tissue engineering or drug delivery. The method provides collagen cross-linked by hydroxyallysine cross-links which are more difficult to cross-linked by hydroxyallysine cross-links which are more difficult to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to a method of obtaining a collagenous matrix which
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         anorectic; cardiant; hypotensive; antiarteriosclerotic; anorectic; virucide; antibacterial; fungicide; protozoacide; notropic; neuroprotective; antiarkinsonian; anticonvulsant; osteopathic; antiarflammatory; dermatological; antiarthmatic; antilipaemic; gene therapy; fibroblast growth factor receptor 4; FGFR4;
                                                                                                                                                                                                                                                                                                                                                                                                                 Obtaining a collagenous matrix with modified resistance against proteolytic degradation, for treating a fibrotic condition, comprises controlling the ratio of hydroxyallysine to allysine cross-links.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  degrade than collagen cross-linked by allysine. The present sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human NOV1 forward real time quantitative PCR primer SEQ ID NO:146.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ss; PCR; primer; real time quantitative PCR; human; antidiabetic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 16.2; DB 1; Length 22;
Pred. No. 1.3e+03;
0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                   Te Koppele JM;
                    tissue engineering; Bruck syndrome; ss; PCR; primer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 22 BP; 10 A; 9 C; 2 G; 1 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                   Bank RA, Van Der Slot AJ, Zuurmond A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2325 GIGIGIGIGIGIGIGIGIG 2345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 3; Page 12; 25pp; English.
                                                                                                                                                                                                                                                                                       (NEDE ) NEDERLANDSE ORG TOEGEPAST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            represents a PLOD2 PCR primer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BP.
                                                                                                                                                                                                  28-JUN-2002; 2002US-00184372.
                                                                                                                                                                                                                                            99US-00450209,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 85.7
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                            WPI; 2004-080749/08.
                                                                                                           US2003219852-A1
                                                                    Homo sapiens.
                                                                                                                                                                                                                                            29-NOV-1999;
                                                                                                                                                       27-NOV-2003
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complement factor I precursor; matrix metalloproteinase-15 precursor; MDC3; T-lymphocyte surface antigen Ly-9 precursor; fibroblast growth factor-21; FGF-21; alpha-2 macroglobulin-like polypeptide variant; antileukoproteinase 1 precursor; LIV-1; nuclear hormone receptor NOR-1; transmembrane protein-like; beta-neoendorphin-dynorphin precursor. 12-SEP-2002; 2002US-0410320P. 16-SEP-2002; 2002US-0411060P. 23-SEP-2002; 2002US-0412766P. 23-SEP-2002; 2002US-0412825P. 24-SEP-2002; 2002US-0413767P. 25-SEP-2002; 2002US-0413342P. 2002US-0409544P. 09-SEP-2003; 2003WO-US028141 30-SEP-2002; 2002US-0414832P WO2004022723-A2. Homo sapiens. 09-SEP-2002; 18-MAR-2004.

New isolated NOVX polypeptides and polynucleotides, useful for preventing, diagnosing or treating NOVX-associated disorders, e.g. osteoarthritis, obesity, atherosclerosis, cancer, Parkinson's disease, asthma, or infections. Ort I, Padigaru M, Rieger DK; Guo X, Anderson DW, WPI; 2004-315567/29. Zhong M,

(CURA-) CURAGEN CORP.

Example 12; SEQ ID NO 146; 214pp; English.

The invention relates to a novel isolated polypeptide (NOVX) comprising a mature form of any of the 37 amino acid sequences fully defined in the specification. A polypeptide of the invention has antidiabetic, antibacterial, fungicide, protozoacide, nootropic, virucide, antibacterial, fungicide, protozoacide, nootropic, or antibacterial, fungicide, protozoacide, nootropic, antiinflammatory, dermatological, antiathmatic, and antibodies cartilipaemic activity. A polymoleckide of the invention may have a use antibacterial, the manufacture of a medicament for treating a syndrome associated with a human disease, preferably a NOVX-associated disorder. The nucleic acid molecules, polypeptides and antibodies are useful in the manufacture of a medicament for treating a syndrome associated with a human disease, preferably a NOVX-associated disorder. CC treating, preventing or diagnosing diseases such as metabolic disorders, cliabetes, obseity, infectious diseases such as metabolic disorders, diabetes, obseity, infectious diseases such as metabolic disorders, cliabetes, parkinson's disease, pilppsy, immune disorders (Nypertension, atherosocialvis), neurodegenerative disorders, asthma, and various disease, epilppsy, immune disorders (osteoarthritis), heematopoietic disorders, inflammatory skin disorders, asthma, and various dyslipidaemias. The nucleic acids and polypeptides constant and parances for use in therapeutic or diapostic acids and polypeptides of the invention sow homology to certain known human crissue typing, prevention show homology to certain known human proteins; NOVIa shows homology to confidence; nowed shows homology to complement factor receptor shows homelogy to shows homology to shows homology to shows homology to matrix metalloroteinase. Disperced shows homology to complement factor receptor shows shows homology to matrix metalloproteinaes-15 precursor; NOV4a shows homology to matrix metalloproteinaes-15 precursor; NOV4a shows homology to WDC3; NOV5a-5c show homology to T-lymphocyte surface antigen Ly-9 precursor; NOV6a-6m show homology to fibroblast growth factor-21 polypeptide variant; NOV9a-8g show homology to alpha-2 macroglobulin-like polypeptide variant; NOV8a-8g show homology to antileukoproteinae 1 precursor; NOV9a-9j show homology to LIV-1 protein; NOV10a shows homology

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Gaps

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suppressive invention describes at rypansor. The present invention suppressive intended that a factor (TSIF) processor. The present invention also describes: (1) the TSIF protein having the primary structural information of amino acids 1-553 of the 813-amino acid sequence of SEQ ID NO:2 (ADP74801) or its fragment or allelic variant having immunomodulating activity, (2) an isolated polymucleotide comprising a 2826 base pair sequence of SEQ ID NO:1 (ADP74800) which encodes the TSIF polypeptide; (3) a vector comprising the nuclaic acid; (4) a genetically engineered host cell comprising the expression vector; and (5) preparing a diagnostic assaay for detecting the presence of a Trypanozoon infection in a mammal. TSIF has immunosuppressive activity, and can be used in gene therapy. The TSIF polypeptide or polynucleotide can be used in preparing a medicament for suppressing the immune response in a mammal for treating autoimmune disorders. The present sequence represents a PCR primer for TSIF, which is used in an example from the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     otide derived from Trypanosomes, useful in preparing a
for suppressing the immune response in a mammal for treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; oestrogen receptor; ligand; bone resorption; metabolic disorder;
                                                                                                                                                                                    TSIF; immunomodulating activity; Trypanozoon infection;
immunosuppressive; gene therapy; immune response; autoimmune disorder;
                                                                                                                                                            trypanosome suppressive immunomodulating factor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention describes a Trypanosoma brucei trypanosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0.4%; Score 16.2; DB 1; Length 22; 35.7%; Pred. No. 1.3e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 22 BP; 4 A; 4 C; 8 G; 6 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human oestrogen receptor gene PCR primer #2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                               brucei TSIF PCR primer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  603 GGTGTACAGTGACGCACAGCC 623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example; Page 28; 54pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22 GGTATACACTGACGCACACCC
                                                                                                                                                                                                                                                                                                                                                                                                                                      19-DEC-2003; 2003WO-EP051082.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23-DEC-2002; 2002EP-00080667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Beschin A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             85.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAX34311 standard; DNA; 23
                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity 85.7
les 18, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New polypeptide derived medicament for suppressi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               autoimmune disorders.
                                                                                                                                                            Trypanosoma brucei;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2004-500278/47
                                                                                                                                                                                                                                                                           Irypanosoma brucei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             De Baetselier P,
                                                                                                                                                                                                                              PCR; primer; ss
                                                                                                                                                                                                                                                                                                                                              WO2004056853-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (VIBV-) VIB VZW
                                                                    23-SEP-2004
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                                                                                                                 Тгураповоща
                                                                                                                                                                                                                                                                                                 Synthetic.
                          ADP74809;
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention relates to a method for identifying an organism using the intron sequence of the clock gene as DNA fingerprints. The method comprises the steps of: constructing a pair of primers for PCR capable of amplifying intron using consecutive nucleotide sequences before and after of the clock gene intron; amplifying intron by PCR using the pair of primers; sequencing the amplified intron DNA fragments; and identifying the organism to analyse the nucleotide sequence of the intron. The present sequence is a PCR primer used in the method of the invention.
to nuclear hormone receptor NOR-1; NOV11a-11j show homology to transmembrane protein-11ke; NOV12a-12c show homology to beta-necendorphin dynorphin precursor. The present sequence represents a PCR primer used in the exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Identification of organism using the intron DNA sequence of the clock gene as DNA fingerprints.
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                                                                                                                                                          0.4%; Score 16.2; DB 1; Length 22; ilarity 85.7%; Pred. No. 1.3e+03; Conservative 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0.4%; Score 16.2; DB 1; Length 22; 85.7%; Pred. No. 1.38+03; ive 0; Mismatches 3; Indels
                                                                                                               Sequence 22 BP; 9 A; 6 C; 4 G; 3 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 22 BP; 4 A; 8 C; 4 G; 6 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Clock gene; DNA fingerprint; PCR; primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Clock gene intron PCR primer, SEQ ID 7.
                                                                                                                                                                                                                                                      1293 CGTGAAGATGCTGAAAGACGA 1313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      992 TGGGCTCCCCCACCGTGCACA 1012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 3; SEQ ID NO 7; 19pp; Korean.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (KOOC-) KOREA OCEAN RES & DEV INST.
                                                                                                                                                                                                                                                                                                 CGTCAAGATGCTCAAAGACAA 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 resecricircacaca
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Les 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                ADQ75599 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2004-105148/11
                                                                                                                                                     Query Match
Best Local Similarity
Matches 18; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lee YH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KR2003075818-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unidentified
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Best Local S:
Matches 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADQ75599
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kim WS,
                                                                                                                                                                                                                                                                                                                                                                   RESULT 940
ADQ75599
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ADP74809/c
ID ADP74
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Indels

ADP74809 standard; DNA; 22 BP

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library for a single chain monoclonal antibody fusion reagent capable of binding a transcriptional associated biomolecule in vivo. The antibodies are useful in treating Hepatitis A and B respiratory syncitial virus, HIV, Junin virus, Herpes simplex I and II, rubella, cytomegalovirus, Varicella-Zoster virus, Epstein-Barr virus, measles, hantavirus, dengue, Ebola inter alia and cancer. Expression vectors that encode the fusion antibodies may be used in gene therapy. The methods can be used to create and isolate the fusion antibodies. The monoclonal antibody fusion reagent can be used to regulate transcription in vivo. AAX76591 to AAX76674 represent specifically claimed PCR primers used in the construction of a human sFv library
                                                                                                                                                                                                  Antibodies from libraries useful in treating viral infections and cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This invention relates to a human gene encoding a capsid protein zeta subunit (zeta-COP). The invention also relates to a zeta-COP protein sequence. The present sequence represents a PCR primer used to amplify
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 16.2; DB 1; Length 23;
Pred. No. 1.4e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel human capsid protein subunit coding sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 23 BP; 3 A; 4 C; 11 G; 5 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (XINH-) XINHUANGPU FUDAN GENE ENG CO LTD SHANGHA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; capsid-protein; zeta-COP; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      874
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                                                                                                                                                                                                                                         Claim 23; Page 81; 132pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 1; Page 9; 21pp; Chinese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PCR primer specific for zeta-COP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        854 AGGAGGAGCTGGTGGAGGCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 AGGTGCAGCTGGTGGAGTCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0.4%;
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    97WO-US021407.
                                           97WO-US021407.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity 85.7 tes 18; Conservative
                                                                                                                      Hoeffler JP, Russell M;
                                                                                 (INVI-) INVITROGEN CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2000-431993/38.
                                                                                                                                                             WPI; 1999-371138/31
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22-SEP-1998;
      28-NOV-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    primers AAX34310-X34312 were used to PCR amplify and isolated cDNA clones encoding a human oestrogen receptor (AAX34309). The receptor can be used to identify ligands that bind to human oestrogen receptor. The ligands can be used in a method for preventing or treating an oestrogen receptor mediated disease or condition, such as abnormal bone resorption, a candidated cardiovascular disease, cancer, metabolic disorders, or central nervous system disorders. The ligand is especially used to treat osteoporosis, breast, uterine, ovarian or prostate cancer, diabetes or Alzheimer's
cardiovascular disease; cancer; central nervous system; breast; uterine; osteoporosis; ovarian; prostate; diabetes; Alzheimer's disease; PCR; primer; amplification; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; sFV library; single chain monoclonal antibody fusion reagent; transcription regulation; screening; diagnosis; HIV; Hepatitis A; Hepatitis B respiratory syncitial virus; Junin virus; cytomegalovirus; Herpes simplex virus; rubella; Varicella-Zoster virus; hantavirus; Epstein-Barr virus; measles; dengue; Ebola inter alia; cancer;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Estrogen receptor useful in ligand identification in medicine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 16.2; DB 1; Length 23;
Pred. No. 1.4e+03;
0; Mismatches 3; Indels
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97US-0060520P.
97GB-00022884.
98GB-0006032.
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Best Local Similarity 85.7%;
Matches 18; Conservative
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                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                               08-SEP-1997;
30-SEP-1997;
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20-MAR-1998;
                                                                                                                                               WO9912961-A1
                                                                                                                                                                                                                             04-SEP-1998;
                                                                                                                                                                                                                                                                                                                                                                                                       Wilkinson H;
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                                                                                      Synthetic
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